

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 6, 2006, 21:44:31 ; Search time 43 Seconds
(without alignments)
693.656 Million cell updates/sec

Title: US-10-736-227-1

Perfect score: 1663
Sequence: 1 MGNQVEKTLHLYKEVETAD.....PPGRPPAPSSSEEDGEAAVAH 310

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

O. nult No.	Score	Query Match	Length	DB ID	Description
1	116	7.0	160	2 S42794	p18H-rev 107 prote
2	102.5	6.2	249	2 A41497	36K antigen pra -
3	102	6.1	1956	2 T00051	hypothetical prote
4	101.5	6.1	673	2 T00328	hypothetical prote
5	98	5.9	419	2 T29286	hypothetical prote
6	97.5	5.9	516	2 H71332	hypothetical prote
7	97.5	5.9	775	2 S55345	protein-tyrosine-P
8	96.5	5.8	1206	2 S24407	formin isoform IV
9	96.5	5.8	1468	2 S11515	formin - mouse
10	95.5	5.7	189	2 AE3327	hypothetical prote
11	95.5	5.7	301	2 E29149	proline-rich prote
12	95.5	5.7	549	2 C87719	protein R119.6 (im
13	94.5	5.7	481	2 T27915	hypothetical prote
14	94.5	5.7	500	2 S64220	hypothetical prote
15	94	5.7	240	2 D70894	probable pra prote
16	93.5	5.6	229	1 W4W18	E4 protein - human
17	93.5	5.6	416	1 W2W1DP	E2 protein - deer
18	93.5	5.6	485	1 A33647	sulfated surface g
19	93	5.6	245	1 W4W15	E4 protein - human
20	92.5	5.6	1952	2 T48814	hypothetical prote
21	92	5.5	171	2 A27307	proline-rich phosp
22	92	5.5	472	1 A49836	transcription fact
23	92	5.5	636	2 T07447	DNA-directed RNA p
24	91.5	5.5	281	2 S65692	E4 protein - human
25	91.5	5.5	508	2 S54264	glycoprotein GC -
26	91.5	5.5	2957	2 T33152	hypothetical prote
27	91	5.5	385	2 H70937	hypothetical prote
28	91	5.5	1239	1 Q08E10	BOLFI protein - hu
29	91	5.5	1692	2 G01449	probable mucin G2

30	90.5	5.4	318	2 T29479	hypothetical prote
31	90.5	5.4	1392	2 T51947	probable transcrip
32	90.5	5.4	2715	2 T13049	eyelid - fruit fly
33	90	5.4	372	2 T14193	L-ascorbate peroxi
34	90	5.4	521	2 A29249	RNA-directed RNA p
35	90	5.4	741	2 I51657	suppressor of yeas
36	89.5	5.4	170	2 A48013	proline-rich prote
37	89.5	5.4	286	1 P1RT3	acidic proline-ric
38	89.5	5.4	204	2 H87524	hypothetical prote
39	89.5	5.4	420	2 T46910	hypothetical prote
40	89.5	5.4	521	1 VGBEBH	glycoprotein gill
41	89.5	5.4	697	1 TVVPTL	large T antigen -
42	89.5	5.4	1018	2 T43168	hypothetical prote
43	89.5	5.4	1029	1 S21369	collagen alpha 2IV
44	89.5	5.4	1259	2 T16038	hypothetical prote
45	89.5	5.4	1638	2 T30313	chemotaxis protein

ALIGNMENTS

RESULT 1

S42794
p18H-rev 107 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42794

R:Schaefer, R.
submitted to the EMBL Data Library, November 1993

A:Reference number: S42794

A:Accession: S42794

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-160 <SCH>

A:Cross-references: UNIPROT:P53817; UNIPARC:UPI000012CE5; EMBL:X76453; NID:9433962; PI

Query Match 7.0%; Score 116; DB 2; Length 160;
Best Local Similarity 31.9%; Pred. No. 0.024;
Matches 38; Conservative 17; Mismatches 36; Indels 28; Gaps 6;

Oy 117 KPGLVFEVSOAQPHNAVYGNFQVHL-----HRLVINSFILTDS----- 159
Db 7 KPGLIE-IFRPMYSHAIYGDGVYHLAPPSIPGAGASIALTKAIVKELLRD 65
Oy 160 -OGRRGRVNDLY--RYKPLSSAVRNALAHGAKRELSWR-----NSSEFAWCRYG 211
Db 66 VAGKDKYQVNNKDKETTPLPNKTIQRAELVG---QEVYRLTSENCEHFVNLRYG 121

RESULT 2

A41497
36K antigen pra - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: A41497

R:Thole, J.E.R.; Stabel, L.F.E.M.; Suykerbuyk, M.E.G.; de Wit, M.Y.L.; Klatter, P.R.; K

Infect. Immun. 58, 80-87, 1990

A:Title: A major immunogenic 36,000-molecular-weight antigen from Mycobacterium leprae

A:Reference number: A41497; PMID:1688422

A:Accession: A41497

A:Molecule type: DNA

A:Residues: 1-249 <THO>

A:Cross-references: UNIPROT:P41484; UNIPARC:UPI000013216A; GB:X65546

Query Match 6.2%; Score 102.5; DB 2; Length 249;
Best Local Similarity 20.4%; Pred. No. 0.54;
Matches 56; Conservative 26; Mismatches 108; Indels 85; Gaps 11;

Oy 17 PTADPTGVDDDDPRIGSVYIFSNDDVDVEPPPPGPGDGGL------PDGSDGPPPP 71
Db 14 PAPPFGSSGGRPPSPAPSELGS-----AYPPFPAPVPGGSPPPPPGSGYPPPPPP 66
Oy 72 QPYDPRLHEVEGVSFYRDECIYOKSFAPGSAALSTYTPENLANKCKRGDLVEFVSOAQP 131

Db 301 EEDGEAVAH 310

RESULT 2

US-10-074-475-267
Sequence 267, Application US/10074475
Publication No. US20030092898A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Hervé
APPLICANT: Kaira, Kaipana
APPLICANT: Cafferey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chonghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
FILE REFERENCE: DEX-0313
CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 295
SOFTWARE: Patentin version 3.1
SEQ ID NO 267
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapien
US-10-074-475-267

Query Match 27.0%; Score 449.5; DB 4; Length 111;
Best Local Similarity 82.9%; Pred. No. 1.6e-32;
Matches 92; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

Qy 168 NDLYRYKPLSSAVRNALAHVGAKEKELSWNSPFAWGVKREKIGGELRIKOP 227
Db 1 NDLYRYKPLSSAVRNALAHVGAKEKELSWNSPFAWGVKREKIGGELRIKOP 60
228 YRLQIQLSAQRSHLTLEFQSLLEDLIM-EKRRNDQIGRAVLOELATHLHPAE 277
Db 61 YRLQIQLSAQRSHLTLEFQSLLEDLIMGEATQPRSGARVLOELATHLHPAE 111

RESULT 3

US-10-104-047-3151
Sequence 3151, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3151
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3151

Query Match 16.2%; Score 269.5; DB 4; Length 354;
Best Local Similarity 32.8%; Pred. No. 1.5e-15;
Matches 76; Conservative 25; Mismatches 80; Indels 51; Gaps 10;

Qy 1 MGNQVEKLTHTLSYKEVPTADPTGVDRDDGPRIGVSYFSNDDVEVEPPQPGDGGGLP 60
Db 1 MGNQVDRITHTLHYSELPTGDPGSGIEKDE-LRVGVAYFFSDDEEDL-----DERGQP 50
61 D--GGDGPPEPPQPGPYDRHL-----EVECSVFYRDECIYOK-SFAPGSAALST 106

Db 51 DKRGVKAPEGCTPCBPSPSRHHHLLHQLVLTETQFAFGQECIFSKVSGPGGADLSV 110

Qy 107 YTEPENTLNKCKPGDLVEFV-----SOAQYPHWAVYVGNFQVVLHRLLEVINSFLTDAS 159

Db 111 YAVTALPALCEPGLLELWLQPAPEPPAPAPHWASPAR-SAGRTRRASPAGALASGS 169

Qy 160 QGRRGVNDLYRYKPLSSAVRNALAHVGAKEKELSWNSPFAWGVKREKIGGELRIKOP 207
Db 170 SRREGRC--ROARSPRSSSTISR-----CTWERTRSTPPGFTAW 206

RESULT 4

US-11-072-512-3151
Sequence 3151, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHINO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3151
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3151

Query Match 16.2%; Score 269.5; DB 6; Length 354;
Best Local Similarity 32.8%; Pred. No. 1.5e-15;
Matches 76; Conservative 25; Mismatches 80; Indels 51; Gaps 10;

Qy 1 MGNQVEKLTHTLSYKEVPTADPTGVDRDDGPRIGVSYFSNDDVEVEPPQPGDGGGLP 60
Db 1 MGNQVDRITHTLHYSELPTGDPGSGIEKDE-LRVGVAYFFSDDEEDL-----DERGQP 50

Qy 61 D--GGDGPPEPPQPGPYDRHL-----EVECSVFYRDECIYOK-SFAPGSAALST 106
Db 51 DKRGVKAPEGCTPCBPSPSRHHHLLHQLVLTETQFAFGQECIFSKVSGPGGADLSV 110

Qy 107 YTEPENTLNKCKPGDLVEFV-----SOAQYPHWAVYVGNFQVVLHRLLEVINSFLTDAS 159
Db 111 YAVTALPALCEPGLLELWLQPAPEPPAPAPHWASPAR-SAGRTRRASPAGALASGS 169

Qy 160 QGRRGVNDLYRYKPLSSAVRNALAHVGAKEKELSWNSPFAWGVKREKIGGELRIKOP 207
Db 170 SRREGRC--ROARSPRSSSTISR-----CTWERTRSTPPGFTAW 206

RESULT 5

```
US-10-450-763-33497
; Sequence 33497, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 33497
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(96)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-33497

Query Match      13.8%; Score 229; DB 5; Length 96;
Best Local Similarity 66.2%; Pred. No. 1.2e-12;
Matches 45; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY      52 GPPDGGGLDGDGPPPPQPPYDPRLHVECSVFYRDCITYKSPAPSAALSTYTPEN 111
      11 RQDMAAACPVTGTCGRPPSRSSYDPRLHVECSVFYRDCITYKSPAPSAALSTYTPEN 70
      112 LUNKCKPG 119
      71 LPOQVQAG 78
DB

RESULT 6
US-10-171-311-198
; Sequence 198, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatz, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-198
```

```
Query Match      8.5%; Score 141; DB 4; Length 164;
Best Local Similarity 32.2%; Pred. No. 0.00021;
Matches 39; Conservative 21; Mismatches 39; Indels 22; Gaps 5;

QY      117 KPGLDVEFVSQAQYPMHVVYVGNFOYVHL-----HRLVINSFLTASQGRG---- 164
      9 KPGLDLE-IFRLGVEHMAVYIGDGYVYHLAPPSEYFGAGSSVFSVLSNBAEYKGRLED 67
DB      165 -----RVVNDL-YRKPGLSSSAVVRNALAHVGAKEE-ELSMRNSESFAAMCRYGKREF 215
      68 VVGCCCYRVNNSLDHEYQRPVEVIISAKENVGQMKYISVRNCEHFVAQLRYGKSRG 127
QY      216 K 216
      128 K 128
DB

RESULT 7
US-10-723-860-3892
; Sequence 3892, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nacasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3892
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-3892

Query Match      8.5%; Score 141; DB 5; Length 164;
Best Local Similarity 32.2%; Pred. No. 0.00021;
Matches 39; Conservative 21; Mismatches 39; Indels 22; Gaps 5;

QY      117 KPGLDVEFVSQAQYPMHVVYVGNFOYVHL-----HRLVINSFLTASQGRG---- 164
      9 KPGLDLE-IFRLGVEHMAVYIGDGYVYHLAPPSEYFGAGSSVFSVLSNBAEYKGRLED 67
DB      165 -----RVVNDL-YRKPGLSSSAVVRNALAHVGAKEE-ELSMRNSESFAAMCRYGKREF 215
      68 VVGCCCYRVNNSLDHEYQRPVEVIISAKENVGQMKYISVRNCEHFVAQLRYGKSRG 127
QY      216 K 216
      128 K 128
DB

RESULT 8
US-10-756-149-5683
; Sequence 5683, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nacasha
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS &
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5683
; LENGTH: 164
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TYPE: PRT
ORGANISM: Homo Sapiens
US-10-756-149-5683

Query Match
Best Local Similarity 32.2%; Score 141; DB 5; Length 164;
Matches 39; Conservative 21; Mismatches 39; Indels 22; Gaps 5;

117 KPGDLVEFVSQAQYPRHMAVYVGNFOVHL-----HRLVINSFLTDSQGRG--- 164
9 KPGDLIE-IFRLGYEHMALYIGDGYVHLAPPSEYPGAGSSSVFSLNSAEVKKRLED 67

165 -----RVVNDL-YRKYPLSSAVVRNALAHVGAKER-ELSWNSESFAAMCRGKREF 215
68 VVGCCYRVNNSLDHEYOPRVEVLISSAKEMVGQMKYISVSRNCEHFTQTALRYGKSR 127

216 K 216
128 K 128

RESULT 9
S-10-020-618-1
Sequence 1, Application US/10020618
Publication No. US20020156256A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: A NOVEL H-REV107-LIKE
PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/020,618
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,742
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0200 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-020-618-1

Query Match
Best Local Similarity 32.2%; Score 136; DB 4; Length 164;
Matches 39; Conservative 15; Mismatches 45; Indels 22; Gaps 4;

117 KPGDLVEFVSQAQYPRHMAVYVGNFOVHL-----HRLVINSFLTD 157
9 KPGDLIE-IFRLGYEHMALYIGDGYVHLAPPSEYPGAGSSSVFSLNSAEVKKRLED 67

158 ASQGRGRVNDL-YRKYPLSSAVVRNALAHVGAKER-ELSWNSESFAAMCRGKREF 215
68 VVGCCYRVNNSLDHEYOPRVEVLISSAKEMVGQMKYISVSRNCEHFTQTALRYGKSR 127

216 K 216
128 K 128

RESULT 10
US-10-616-942-2
Sequence 2, Application US/10616942
Publication No. US20040048339A1
GENERAL INFORMATION:
APPLICANT: Kato, Seishi
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND
FILE REFERENCE: GIN-6710CPUS
CURRENT APPLICATION NUMBER: US/10/616,942
FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US/09/529,100
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: JP 0276269
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: PCT/JP98/04474
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapiens
US-10-616-942-2

Query Match
Best Local Similarity 32.2%; Score 136; DB 4; Length 164;
Matches 39; Conservative 15; Mismatches 45; Indels 22; Gaps 4;

117 KPGDLVEFVSQAQYPRHMAVYVGNFOVHL-----HRLVINSFLTD 157
9 KPGDLIE-IFRLGYEHMALYIGDGYVHLAPPSEYPGAGSSSVFSLNSAEVKKRLED 67

158 ASQGRGRVNDL-YRKYPLSSAVVRNALAHVGAKER-ELSWNSESFAAMCRGKREF 215
68 VVGCCYRVNNSLDHEYOPRVEVLISSAKEMVGQMKYISVSRNCEHFTQTALRYGKSR 127

216 K 216
128 K 128

RESULT 11
US-10-616-942-16
Sequence 16, Application US/10616942
Publication No. US20040048339A1
GENERAL INFORMATION:
APPLICANT: Kato, Seishi
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND
FILE REFERENCE: GIN-6710CPUS
CURRENT APPLICATION NUMBER: US/10/616,942
FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US/09/529,100
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: JP 0276269
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: PCT/JP98/04474
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapiens
US-10-616-942-16

Query Match
Best Local Similarity 8.2%; Score 136; DB 4; Length 164;
Matches 39; Conservative 15; Mismatches 45; Indels 22; Gaps 4;

QY 117 KPGDIVEFSAQYPMHAYVGNFOYVHL-----HRLVINSFLTD 157
DB 9 KPGDIE-IFRLGYHEMALYIDGVYIHLAPPEYVPGACSSVFSVLSNAAVEKRELEDD 67
QY 158 ASQGRGRVNDL-TRYKPLSSAVVRNMLAHVAKER-ELSMRNSFSAACRGKREF 215
DB 68 VVGCCYRVNNSLDHEOPEVPEVITISSAKENVGQMKYSIVSRNCEHFVTLRYGKSRG 127
QY 216 K 216
DB 128 K 128

RESULT 12
US-10-116-326-6

Sequence 6, Application US/10116326
Publication No. US20030166889A1

GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Mathur, Brian
APPLICANT: Fiedler, Carl Johan

TITLE OF INVENTION: No. US20030166889A1 Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0332-USA

CURRENT APPLICATION NUMBER: US/10/116,326
CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 60/282,036
PRIOR FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6
LENGTH: 703
TYPE: PRT

ORGANISM: homo sapiens
US-10-116-326-6

Query Match
Best Local Similarity 7.3%; Score 122; DB 4; Length 703;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;

QY 50 PPGPDGGGLPDGDPGPPPPQ-----PPYDP----- 76
DB 404 PSRGRGGG---AGQPPPPSARSTPLPGPPSSGGTPLHPLTPRASPTGPGTT 460
QY 77 -----RLHEVCSVYRDECTYQKSAFAGSALSTYTPENLKNCKPGD 120
DB 461 PPPSPGGVGGAAMSRNLSINRSLGSPRRFRKQVPTAEEMSLTPESSEPELAKRS- 519
QY 121 LVEFVSQAYPMHAYVGNFOYVHLHRLVINSFLTDSQGRGRVNDLYRYKPLSSA 180
DB 520 -----WFGNF--ISLDKEQITLVLDK-----KPLSS-- 544
QY 181 VVRNALAHVAKERELSWR--NSESFAAMCRYGKEFKIGELRGKOPYRLOIOLSAOR 238
DB 545 -IKADIVAFSLPSLSHVSLSQTSFRA-----EYRASGSPSVFOKRVKQVVISSE 596
QY 239 S-----HTLEFQSLDLMKRRNDQIGRAAVLQELATLHHPAEPEGD- 282
DB 597 GPSPRRDGGGGGIGYVTFLLISG---PSRRFRKVVETIOALLSTHDPSVOLADE 653
QY 283 SNVART-----TPPGRP--PAPSEEDG 305
DB 654 KNGAOTRPAAGAPRRSLQPPGGRPDELSSSPRRG 687

RESULT 13
US-10-803-277-6

Sequence 6, Application US/10803277
Publication No. US20040180416A1

GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Mathur, Brian
APPLICANT: Fiedler, Carl Johan

TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0332-USA

CURRENT APPLICATION NUMBER: US/10/803,277
CURRENT FILING DATE: 2004-03-18

PRIOR APPLICATION NUMBER: US/10/116,326
PRIOR FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 60/282,036
PRIOR FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6
LENGTH: 703
TYPE: PRT

ORGANISM: homo sapiens
US-10-803-277-6

Query Match
Best Local Similarity 7.3%; Score 122; DB 4; Length 703;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;

QY 50 PPGPDGGGLPDGDPGPPPPQ-----PPYDP----- 76
DB 404 PSRGRGGG---AGQPPPPSARSTPLPGPPSSGGTPLHPLTPRASPTGPGTT 460
QY 77 -----RLHEVCSVYRDECTYQKSAFAGSALSTYTPENLKNCKPGD 120
DB 461 PPPSPGGVGGAAMSRNLSINRSLGSPRRFRKQVPTAEEMSLTPESSEPELAKRS- 519
QY 121 LVEFVSQAYPMHAYVGNFOYVHLHRLVINSFLTDSQGRGRVNDLYRYKPLSSA 180
DB 520 -----WFGNF--ISLDKEQITLVLDK-----KPLSS-- 544
QY 181 VVRNALAHVAKERELSWR--NSESFAAMCRYGKEFKIGELRGKOPYRLOIOLSAOR 238
DB 545 -IKADIVAFSLPSLSHVSLSQTSFRA-----EYRASGSPSVFOKRVKQVVISSE 596
QY 239 S-----HTLEFQSLDLMKRRNDQIGRAAVLQELATLHHPAEPEGD- 282
DB 597 GPSPRRDGGGGGIGYVTFLLISG---PSRRFRKVVETIOALLSTHDPSVOLADE 653
QY 283 SNVART-----TPPGRP--PAPSEEDG 305
DB 654 KNGAOTRPAAGAPRRSLQPPGGRPDELSSSPRRG 687

RESULT 14
US-10-204-639-65

Sequence 65, Application US/10204639
Publication No. US20060063152A1

GENERAL INFORMATION:
APPLICANT: Osamu Ohara
APPLICANT: Takahiro Nagase
APPLICANT: Daisuke Nakajima

TITLE OF INVENTION: NOVEL GENE AND PROTEIN ENCODED BY THE GENE
FILE REFERENCE: PH-1416-PCT

CURRENT APPLICATION NUMBER: US/10/204,639
CURRENT FILING DATE: 2002-08-22

PRIOR APPLICATION NUMBER: JP 2000-389742
PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: JP 2001-095524
PRIOR FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: JP 2001-127066
PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 140

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OM protein - protein search, using sw model

Run on: December 6, 2006, 21:51:21 : Search time 40 Seconds

(without alignments)
699.504 Million cell updates/sec

Title: US-10-736-227-1

Perfect score: 1663
Sequence: 1 MGNVEKTLTHSYKEVPTAD.....PGRPPAPSSSEDEGNAVAH 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 358988 seqs, 90258633 residues

Total number of hits satisfying chosen parameters: 358988

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA New:*

- 1: /EMC_Celerra_SIDS3/prodata/1/pubppa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/1/pubppa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/1/pubppa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/1/pubppa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/1/pubppa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US00_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1663	100.0	310	US-10-527-788-63	Sequence 63, Appl
2	642.5	38.6	292	US-10-527-788-64	Sequence 64, Appl
3	282	17.0	63	US-10-527-788-23	Sequence 23, Appl
4	282	17.0	63	US-10-527-788-34	Sequence 34, Appl
5	141	8.5	164	US-10-533-519-822	Sequence 822, Appl
6	122	7.3	794	US-11-320-072-74	Sequence 74, Appl
7	115.5	6.9	872	US-10-613-783-4430	Sequence 4430, Appl
8	101.5	6.1	328	US-10-131-833A-364	Sequence 364, Appl
9	97.5	5.9	854	US-10-449-902-41174	Sequence 41174, Appl
10	94.5	5.7	543	US-10-953-349-21087	Sequence 21087, Appl
11	94.5	5.7	586	US-10-953-349-21086	Sequence 21086, Appl
12	94.5	5.7	1453	US-11-056-355B-81762	Sequence 81762, Appl
13	94.5	5.7	1661	US-11-056-355B-81761	Sequence 81761, Appl
14	94.5	5.7	1714	US-11-056-355B-81760	Sequence 81760, Appl
15	93.5	5.6	326	US-11-056-355B-1197	Sequence 1197, Appl
16	93.5	5.6	326	US-10-449-902-40809	Sequence 40809, Appl
17	93	5.6	1081	US-10-612-783-6929	Sequence 6929, Appl
18	92.5	5.6	270	US-10-953-349-26560	Sequence 26560, Appl
19	92.5	5.6	270	US-11-056-355B-63759	Sequence 63759, Appl
20	92.5	5.6	309	US-10-953-349-26559	Sequence 26559, Appl
21	92.5	5.6	309	US-11-056-355B-63758	Sequence 63758, Appl
22	92.5	5.6	357	US-10-449-902-50208	Sequence 50208, Appl
23	92.5	5.6	447	US-10-539-228-684	Sequence 684, Appl
24	92	5.5	567	US-10-449-902-45116	Sequence 45116, Appl
25	92	5.5	1015	US-10-553-520-132	Sequence 132, Appl

26	91.5	5.5	773	US-10-539-228-845	Sequence 845, Appl
27	91	5.5	597	US-11-043-842-765	Sequence 765, Appl
28	91	5.5	597	US-11-362-260A-173	Sequence 173, Appl
29	90.5	5.4	849	US-10-953-349-1432	Sequence 1432, Appl
30	90.5	5.4	1003	US-10-953-349-1431	Sequence 1431, Appl
31	90.5	5.4	1392	US-10-953-349-1430	Sequence 1430, Appl
32	90.5	5.4	1616	US-10-533-519-52	Sequence 52, Appl
33	90	5.4	346	US-10-953-349-34821	Sequence 34821, Appl
34	90	5.4	346	US-11-056-355B-1723	Sequence 4723, Appl
35	90	5.4	347	US-11-056-355B-73930	Sequence 73930, Appl
36	90	5.4	348	US-10-953-349-6363	Sequence 6363, Appl
37	90	5.4	348	US-11-056-355B-25741	Sequence 25741, Appl
38	90	5.4	348	US-11-056-355B-35941	Sequence 35941, Appl
39	90	5.4	348	US-11-056-355B-105997	Sequence 105997, Appl
40	90	5.4	348	US-11-056-355B-117236	Sequence 117236, Appl
41	90	5.4	352	US-11-056-355B-73949	Sequence 73949, Appl
42	90	5.4	353	US-11-056-355B-25740	Sequence 25740, Appl
43	90	5.4	372	US-10-953-349-6362	Sequence 6362, Appl
44	90	5.4	372	US-11-056-355B-35940	Sequence 35940, Appl
45	90	5.4	372	US-11-056-355B-105996	Sequence 105996, Appl

ALIGNMENTS

RESULT 1
US-10-527-788-63
Sequence 63, Application US/10527788

Publication No. US20060172300A1

GENERAL INFORMATION:

US-10-527-788-63

Query Match 100.0%; Score 1663; DB 6; Length 310;

Best Local Similarity 100.0%; Pred. No. 1.5e-125;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGNVEKTLTHSYKEVPTADPTGVDRDDPGPIGYSYFSNDEDEVEPPPOGGGGLP	60
DB	1	MGNVEKTLTHSYKEVPTADPTGVDRDDPGPIGYSYFSNDEDEVEPPPOGGGGLP	60
QY	61	DGGGPPPOPPQPPDPRLHEVEGCVFTRDECTYKSFAPGSAALSTYPPENLKKCKPGD	120
DB	61	DGGGPPPOPPQPPDPRLHEVEGCVFTRDECTYKSFAPGSAALSTYPPENLKKCKPGD	120
QY	121	LVEFVSQAQYDHWAVVYGNFQVHLHRLVINSFLTJASQGRGRVNVNDLYRYKPLSSA	180
DB	121	LVEFVSQAQYDHWAVVYGNFQVHLHRLVINSFLTJASQGRGRVNVNDLYRYKPLSSA	180
QY	181	VVRNALAHVGAKRELKSRNSESFAWCRYKREFKIGELRIKOPRILOISAOSSH	240
DB	181	VVRNALAHVGAKRELKSRNSESFAWCRYKREFKIGELRIKOPRILOISAOSSH	240

QY 241 TLEFQSLIEDLIMEKRRNDQIGRAAVLOELATHLHPAPEDEGDSNVARTTTPPGRPAPSS 300
DB 241 TLEFQSLIEDLIMEKRRNDQIGRAAVLOELATHLHPAPEDEGDSNVARTTTPPGRPAPSS 300
QY 301 EEDDEGAVAH 310
DB 301 EEDDEGAVAH 310

RESULT 2

US-10-527-788-64
Sequence 64, Application US/10527788
Publication No. US20060172300A1

GENERAL INFORMATION:
APPLICANT: WOLF, SABINE
APPLICANT: JAGER, MARTINA
APPLICANT: BANGSOM, THORSTEN
APPLICANT: BANGSOM, CARMEN
APPLICANT: JORDAN, DOMINIK
APPLICANT: PELZER, BERNHARD
APPLICANT: OPOLZER, THOMAS
TITLE OF INVENTION: METHOD FOR IDENTIFYING BBB-SPECIFIC PROTEINS AND
FILE REFERENCE: 63047(45107)
CURRENT APPLICATION NUMBER: US/10/527,788
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/EP03/09968
PRIOR FILING DATE: 2003-03-08
PRIOR APPLICATION NUMBER: DE 102 42 016.5
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 64
LENGTH: 292
TYPE: PRT
ORGANISM: Homo sapiens
US-10-527-788-64

Query Match 38.6%; Score 642.5; DB 6; Length 292;
Best Local Similarity 46.4%; Pred. No. 7e-44;
Matches 137; Conservative 36; Mismatches 87; Indels 35; Gaps 7;

QY 1 MGNQVEGLTLSTYKEVPTADPTGVDGDDGRIGISYIFSNDDVEVEQPFGGDDGGLP 60
DB 1 MGNQVLDITLHNLSELPTGDPGIGKDE-LRVGVAFPSDEEDL-----DERGQP 50
QY 61 D--GGDPPPPQPPQVPRLL-----EVECSVFYRDECTIYOK-SFAPGSALST 106
DB 51 DKRGVAKAPPGCTPCPESPSPRHQHLHLQVLNLTQFSAFGQECIFSKVSGPGADLSV 110
QY 107 YTPENLKKKPGDLEFV-----SOAQPMAVYVGNFQVVLHRLLEVINSPLTAS 159
DB 111 YATATAPALCEPGLLELMLQAPBPPAPAPAHVAVVGGQIHLHQGEIRQDSTLEAG 170
QY 160 QGRGRVNDLYRKXPSSSAVYNALAHVAKKRELSMRSESFAMCRGKKEFTIGG 219
DB 171 AAVNVRVNVSMYRPLVAELVONACGHLGLKKEEICMTNSESFAAMCRGKKEFTAGG 230
QY 220 ELRIKQP-----YALQIOLSAORSHTEFQSLIEDLIMEKRRNDQIGRAAVLOELA 270
DB 231 EVFAGTQPPQOQYLYLKHLEGNKVTARFHSLEDLIMEKRRIDASGLRVLOELA 285

RESULT 3

US-10-527-788-23
Sequence 23, Application US/10527788
Publication No. US20060172300A1

GENERAL INFORMATION:
APPLICANT: WOLF, SABINE
APPLICANT: JAGER, MARTINA
APPLICANT: BANGSOM, THORSTEN
APPLICANT: BANGSOM, CARMEN

APPLICANT: JORDAN, DOMINIK
APPLICANT: PELZER, BERNHARD
APPLICANT: OPOLZER, THOMAS
TITLE OF INVENTION: METHOD FOR IDENTIFYING BBB-SPECIFIC PROTEINS AND
FILE REFERENCE: 63047(45107)
CURRENT APPLICATION NUMBER: US/10/527,788
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/EP03/09968
PRIOR FILING DATE: 2003-03-08
PRIOR APPLICATION NUMBER: DE 102 42 016.5
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 23
LENGTH: 63
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Partial
amino acid sequence of NSE2 from swine
US-10-527-788-23

Query Match 17.0%; Score 282; DB 6; Length 63;
Best Local Similarity 85.7%; Pred. No. 7.9e-16;
Matches 54; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 248 EDLIMEKRRNDQIGRAAVLOELATHLHPAPEDEGDSNVARTTTPPGRPAPSSSEEDGEA 307
DB 1 EDLIMEKRRNDQIGRAAVLOELATHLHPAPEDEGDSNVARTTTPPGRPAPSSSEEDGEA 60

QY 308 VAH 310
DB 61 VVH 63

RESULT 4

US-10-527-788-34
Sequence 34, Application US/10527788
Publication No. US20060172300A1

GENERAL INFORMATION:
APPLICANT: WOLF, SABINE
APPLICANT: JAGER, MARTINA
APPLICANT: BANGSOM, THORSTEN
APPLICANT: BANGSOM, CARMEN
APPLICANT: JORDAN, DOMINIK
APPLICANT: PELZER, BERNHARD
APPLICANT: OPOLZER, THOMAS
TITLE OF INVENTION: METHOD FOR IDENTIFYING BBB-SPECIFIC PROTEINS AND
FILE REFERENCE: 63047(45107)
CURRENT APPLICATION NUMBER: US/10/527,788
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/EP03/09968
PRIOR FILING DATE: 2003-03-08
PRIOR APPLICATION NUMBER: DE 102 42 016.5
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 34
LENGTH: 63
TYPE: PRT
ORGANISM: Sus sp.
US-10-527-788-34

Query Match 17.0%; Score 282; DB 6; Length 63;
Best Local Similarity 85.7%; Pred. No. 7.9e-16;
Matches 54; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 248 EDLIMEKRRNDQIGRAAVLOELATHLHPAPEDEGDSNVARTTTPPGRPAPSSSEEDGEA 307
DB 1 EDLIMEKRRNDQIGRAAVLOELATHLHPAPEDEGDSNVARTTTPPGRPAPSSSEEDGEA 60

Qy 308 VAH 310
Db 61 VVH 63

RESULT 5

US-10-533-519-822
Sequence 822, Application US/10533519
Publication No. US20060283774A1
GENERAL INFORMATION:
APPLICANT: CLARK, HILARY
APPLICANT: SCHOENFELD, JILL
APPLICANT: VANLOOKEREN, MENNO
APPLICANT: WILKINS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF THE TREATMENT OF IMMUNE
FILE REFERENCE: P1984R1 US
CURRENT APPLICATION NUMBER: US/10/533,519
PRIOR FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: PCT/US03/34312
PRIOR FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 60/423,394
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 2517
SEQ ID NO 822
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
US-10-533-519-822

Query Match 8.5%; Score 141, DB 6, Length 164;
Best Local Similarity 32.2%; Pred. No. 0.00049;
Matches 39; Conservative 21; Mismatches 39; Indels 22; Gaps 5;

Qy 117 KGGDLVEFQAQYPMHVVGNFQVHL-----HRLVINSFLTDSQGRG---- 164
Db 9 KGGDLIE-IFRLCYEHMALYIGGYIHLAPSEYEGAGSSVSFVLSNAEYKRGLED 67
Qy 165 -----RVVNDL-YRKYPLSSSAVVRNALAHYAKER-ELSWRNSESFAMCRYCKREF 215
Db 68 VVGCCCYRVNNSLDHEHYQPRPEVILISSAKENVGQMKYSIVGRNCHEFYAQLRYGKSRG 127
Y 216 K 216
Db 128 K 128

RESULT 6

US-11-320-072-74
Sequence 74, Application US/11320072
Publication No. US20060216730A1
GENERAL INFORMATION:
APPLICANT: PLOMMAN, GREGORY D.
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERRARD
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: MARTINEZ, RICARDO
APPLICANT: FLANAGAN, PETER
APPLICANT: CLARY, DOUGLAS
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
TITLE OF INVENTION: ENZYMS
FILE REFERENCE: 034536-2157
CURRENT APPLICATION NUMBER: US/11/320,072
PRIOR FILING DATE: 2005-12-29
PRIOR APPLICATION NUMBER: 10/130,978
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: PCT/US00/32085
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/167,482
PRIOR FILING DATE: 1999-11-24
PRIOR APPLICATION NUMBER: 60/168,997

PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/174,185
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/178,078
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/179,364
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/183,173
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/187,150
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/190,162
PRIOR FILING DATE: 2000-03-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentln Ver. 3.3
SEQ ID NO 74
LENGTH: 794
TYPE: PRT
ORGANISM: Homo sapiens
US-11-320-072-74

Query Match 7.3%; Score 122, DB 7, Length 794;
Best Local Similarity 21.6%; Pred. No. 0.11;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;

Qy 50 PPGPGGGLPDCGDDPPPPQ-----PPYDP----- 76
Db 495 PSRGPGRGG---AGEPPPSASRSTPLPGPPSPSSGGTPLHSPHTTPASPTGPTT 551
Qy 77 -----RLHVECSVFYRDECITYOKSFAPGSAALSTYTPENLTKKPCPD 120
Db 552 PPPSPGGCVGGAWRRLNSIRNPSFLGSPRFHARKQVTPAEEMSLTPSSPELAKRS- 610
Qy 121 LVEFVSQAQYPMHVVGNFQVHLHRLVINSFLTDSQGRGVRVNDLYRKYPLSSSA 180
Db 611 -----WFGNF--ISLDKEQIFVLKD-----KPLSS-- 635
Qy 181 VVRNALAHYAKERELSMR--NSESFAWRYKREBFKIGELRICKOPYRLOIOISAOR 238
Db 636 -IKADIVHAPLISPLSHSVLSQTSFRA-----BYKSGGSPVQKPYRFQVDISSSE 687
Qy 239 S-----HTLEFOSLEDLIMEKRNDQIGRAAVLQELATHLHPAEPBGD- 282
Db 688 GPEPSPRDGGGGGGLYVTFILISG---PSRRFKRVERIQQLSTHDQPEVQALADE 744
Qy 283 SNVART-----TPPPGRP-PAPSSSEEDG 305
Db 745 KNGAQTRPAGAPPRLSLQPPGRDPPLSSSPRKG 778

RESULT 7

US-10-612-783-4430
Sequence 4430, Application US/10612783
Publication No. US20060236419A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(53373)A
CURRENT APPLICATION NUMBER: US/10/612,783
PRIOR FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 4430
LENGTH: 872
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(872)

OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4577_125772C.1.pcp
US-10-612-783-4430

Query Match 6.9%; Score 115.5; DB 6; Length 872;
Best Local Similarity 21.1%; Pred. No. 0.41;
Matches 85; Conservative 54; Mismatches 123; Indels 141; Gaps 20;

QY 3 NOVEKLTHLSYK-----VPTADPTGVDRDDGPRIGSVYIFSNDEDEVEPQPQPGDG 57
DB 429 HEIDEDSHRSHMEBEGHYEKDMQDEVDVADBDKYE-----SDNRELKPEKXVGPPLG 483
QY 58 GLPDGDDGPPPPQ-----PPYDPRLHEVCSVFPYRDECTYKSFAPGSA 103
DB 484 SAAPFGRRPARPRRGLVCPFDILGVDPKPFDPKTY-VEEDVFVTDESGTKRIRLEDNI 542
QY 104 LSTTTPENL--LNKCKRGDLVEFVSQOYPHW-----AVVVGNOVVAHLRLLEINSFLT 156
DB 543 VRWRTJNNADGTTSC-----SNARFVKMKDGTNQLIGN-----EVLDISVH 585
Y 157 DASQGR-----RGRVNDLYRYKPLSSAVVNALAHV----- 189
586 EAHHDQSHLFLRHKGKILQSGRLHKM-RFMPSSLSKSHRLTLALVDSQNKKTVMQK 644
QY 190 -----GAXERELSWRNSESFAMCCKYGRKEKIGELRIGQYRLOLSAQR 238
DB 645 WFTKDEKAKMEKERYIG-QNIRAHSLQR--KRE-KVN--RKYTOPAPRRQLSP-- 695
QY 239 SHLEFQSLDLIME-----KRNQOIGRAVLQELATHLHPAEBEEDSN 284
DB 696 -----GFLEDALEDEDEPGYSRRMPGRRFEDLEALAEERRIINAK-----KSN 742
QY 285 VARTTP-----PPGRPP-----APSSSEEDGEAVAH 310
DB 743 MSRRVPHKPPYPPPARPPRQADEVSGSEBSESEYETGEDIEH 785

RESULT 8

US-10-131-833A-364
Sequence 364, Application US/10131833A
Publication No. US20060257971A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gettitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C142
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/40/131.833A
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 364
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-833A-364

Query Match 6.1%; Score 101.5; DB 6; Length 328;
Best Local Similarity 28.5%; Pred. No. 1.7;
Matches 73; Conservative 24; Mismatches 72; Indels 87; Gaps 19;

QY 59 LPQDGDGPPPPQPPY-DPRLHEVCSVFPYRDECTYKSFAPGSAALSTYPPENLNKCK 117
DB 14 LRHQAQKPSFSDGPFHQGRVHQA-----APLSDA----- 43
QY 118 PGDLVEFVSQOYPHWAVVYVGNFQVVAHLRL--EVINSF--LT-DASQGRGRVNDLYR 172
DB 44 -----PHDDAH-GNFQYDHEAFLGREVAKEFQDLTPBESQARLGRIVDRMDR 89
QY 173 Y--KPLSSAVVNALAHYAKERELSWRNSESFAMCCKYGRKEKIG-GEIRIGQP 227
DB 90 AGDDGCVSLAEIRAWIAH--TQQRH--RDSVS-AAWDYTDYDRDGRVGEELR----- 139
QY 228 YRLQIQLSAQRSHTL--EFQSLD-----LIMEKR--NDQIGRA-AVLQELATHL 273
DB 140 -----NATYGHAPBEEFHVDVDAETKYKMLARDERRRVVADQDDSDMATRELTAF 192
QY 274 HPAE-PEEGDSNVART 288
DB 193 HPEEPHMRDVIYAET 208

RESULT 9

US-10-449-902-41174
Sequence 41174, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-Oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449.902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41174
LENGTH: 854
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-41174

Query Match 5.9%; Score 97.5; DB 6; Length 854;
Best Local Similarity 20.5%; Pred. No. 11;
Matches 70; Conservative 37; Mismatches 127; Indels 107; Gaps 16;

OY 13 YKEVPTADPTGVDRDDGPRIGSVYIFSNDEDEVEPQPPGCGGLPDC-GDGPPEPPQ 71
DB 151 YRPNPTIN-TSVQSMQGGPSGL-----PAQSSLPFGVGNHPRAASP 190
OY 72 -----QPYDRLHEVECSVFYRDECIYOKSFARG-SAALSTYPPENLNKCKPGDLVE 123
DB 191 ISGPIVASAPY-----SSNACGASISNMAFPFRPRSTSTSGPDTH 230
OY 124 FVS-----QAQYPRMAVYVGNFQVHLHRLVINSFLTASQGRGRVNDLYR 172
DB 221 TVSSVTASQHVAVMAQSHSSIGPOQHOMIGSPILNOSPTLEHGAPGES----- 281
OY 173 YKPLSSAVVRNALAHVAKERELSMRNSSEFAAMRYCKREFK--IGSELATIGQPYRL 230
DB 282 ---TPSLTQSQFVH-GTRDRERSRDSATPG---GRNTFKSVFGFVNSMDSVFA 331
OY 221 Q--IOLSAQ-----RSHTLFQSL-----EDLIMEK--RRNDQIGRAVLOELAT 271
DB 332 OKKITSTPYDPVHLTHVGFNSDTGFTGLPKEMOOLLOESGISRDQANQAVMDIVA 391
OY 272 HLHPAPEEGSDSNAR-----TTPPGCRPPAPSSSEEDG 305
DB 392 FYQDATKSDGPTDVMKMGVAKGNNOAFTPTDITSSDDG 432

RESULT 10

US-10-953-349-21087
; Sequence 21087, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21087
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Glycine max
; US-953-349-21087

Query Match 5.7%; Score 94.5; DB 6; Length 543;

Best Local Similarity 20.4%; Pred. No. 11;
Matches 78; Conservative 41; Mismatches 127; Indels 137; Gaps 16;

OY 18 TADPTGVDRDDGPRIGSVYIFSNDEDEVEPQ-----PQGPDCGGLPDGDDGP--- 67
DB 80 TVATQGMARPETPGIS-SYKMGKTPEVTSSPVAVAGTSPPSAQBGFSGSNVARRPGQY 138
OY 68 PQPQ-----QPYDRLHEVECSVFYRDECIYOKSFAP-----GSAALS 105
DB 139 PASPIKSSDQLVKDSKRVASVNGSSDSFPGGDLFSASSFQKQASSPQGRSSGTSALS 198
OY 106 -----TYPPENLNKCKPGDLVEFVSQAQYPRMAVYVGNFQVHLHRLV 150
DB 199 SAIVPVGNGQSTRTSTPDSLQSLATQPVGAQLQQAQ-----PVVKQDQHAS 247
OY 151 INSFLTASQGRGRVNDLYRKPILSSAVVRNALAHVAKERELSMRNSSEFAAMCR- 209
DB 248 VQTHNKPNSGGLPGR-----LQDSA-----SSQSQAPWPRM 278
OY 210 -----YGK-----REFKIGGE-----LRIGQPYRLQIQLSAQSHTLEFOS 246
DB 279 TQTDVQKWKVMEVDTDRDGKITGEQARNLFLSMRLPREVLKQVMDLSDQNDMSH--LS 336
OY 247 LEDL-----IMEKRNDQIGRAA---VLOELATHLHPA-----EPEEGDS 283
DB 337 LRFECIALYLMERHREGRLPAVLPSNIVLDLPTTGQPAAHYSSMGNPSAFOQDPPTGDS 396

OY 284 NVARTTPPPRPPAPSSSEEDGE 306
DB 397 GARQVNPAGRRPPRAAVSQSDE 419

RESULT 11

US-10-953-349-21086
; Sequence 21086, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21086
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-21086

Query Match 5.7%; Score 94.5; DB 6; Length 586;

Best Local Similarity 20.4%; Pred. No. 12;
Matches 78; Conservative 41; Mismatches 127; Indels 137; Gaps 16;

OY 18 TADPTGVDRDDGPRIGSVYIFSNDEDEVEPQ-----PQGPDCGGLPDGDDGP--- 67
DB 123 TVATQGMARPETPGIS-SYKMGKTPEVTSSPVAVAGTSPPSAQBGFSGSNVARRPGQY 181
OY 68 PQPQ-----QPYDRLHEVECSVFYRDECIYOKSFAP-----GSAALS 105
DB 182 PASPIKSSDQLVKDSKRVASVNGSSDSFPGGDLFSASSFQKQASSPQGRSSGTSALS 241
OY 106 -----TYPPENLNKCKPGDLVEFVSQAQYPRMAVYVGNFQVHLHRLV 150
DB 242 SAIVPVGNGQSTRTSTPDSLQSLATQPVGAQLQQAQ-----PVVKQDQHAS 290
OY 151 INSFLTASQGRGRVNDLYRKPILSSAVVRNALAHVAKERELSMRNSSEFAAMCR- 209
DB 291 VQTHNKPNSGGLPGR-----LQDSA-----SSQSQAPWPRM 321
OY 210 -----YGK-----REFKIGGE-----LRIGQPYRLQIQLSAQSHTLEFOS 246
DB 322 TQTDVQKWKVMEVDTDRDGKITGEQARNLFLSMRLPREVLKQVMDLSDQNDMSH--LS 379
OY 247 LEDL-----IMEKRNDQIGRAA---VLOELATHLHPA-----EPEEGDS 283
DB 380 LRFECIALYLMERHREGRLPAVLPSNIVLDLPTTGQPAAHYSSMGNPSAFOQDPPTGDS 439
OY 284 NVARTTPPPRPPAPSSSEEDGE 306
DB 440 GARQVNPAGRRPPRAAVSQSDE 462

RESULT 12

US-11-056-355B-81762
; Sequence 81762, Application US/11056355B
; Publication No. US20060150283A1

GENERAL INFORMATION:

APPLICANT: Brovet, Vyacheslav
APPLICANT: Alexandrov, Nikolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81762

LENGTH: 1453
TYPE: prt
ORGANISM: Arabidopsis thaliana
NAME/KEY: peptide
LOCATION: (1)..(1453)
OTHER INFORMATION: Ceres Seq. ID no. 12661234
US-11-056-355B-81762

Query Match 5.7%; Score 94.5; DB 7; Length 1453;
Best Local Similarity 23.2%; Pred. No. 37;
Matches 59; Conservative 25; Mismatches 83; Indels 87; Gaps 14;

QY 3 NOVEK-----LTHSYKEVPTADPTGVDRDGPRIQVSYFNSNDEDEVEPOPP-----Q 52
DB 1108 NSVEKGSRRILQQQKEVLPALPS-----GSLGDFVLMKGSVN---NPPAAAMSS 1158
QY 53 GPDGCGLPDG-----GDGPPPOPOP-----YDPRLHEVCSVYRDECIYOK 95
DB 1159 GPKKSTPSSLRDIVKEQEKTTSSHPPSPVPTQKAIPQAHQCGAS-----WSR 1210
Y 96 SFAPGSAALSTYPTENLNCKCPGD-----LVEFVSGAOYPHNAVYVGNFQVHLH 146
1211 SASPSQAVSQSSSQ---SKSGDDDLFWGPEVQSTQDTKQGDPPH----- 1253
Y 147 RLEVINSLTDASQGRGRVNV---DLRYKPLS-----SSAVRNALAHGAKERE 195
DB 1254 -LTSQNSWGKNTKTPGK---VNAQSLNRQKSVMSGADRYLSSPVVTQA-SHGKKEAV 1307
QY 196 LSWRNSESFAAWCR 209
DB 1308 TKLTEANGFRDWCCK 1321

RESULT 13

US-11-056-355B-81761
Sequence 81761, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ. ID NOS: 119966
SEQ. ID NO 81761
LENGTH: 1661
TYPE: prt
ORGANISM: Arabidopsis thaliana
NAME/KEY: peptide
LOCATION: (1)..(1661)
OTHER INFORMATION: Ceres Seq. ID no. 12661233
US-11-056-355B-81761

Query Match 5.7%; Score 94.5; DB 7; Length 1661;
Best Local Similarity 23.2%; Pred. No. 43;
Matches 59; Conservative 25; Mismatches 83; Indels 87; Gaps 14;

QY 3 NOVEK-----LTHSYKEVPTADPTGVDRDGPRIQVSYFNSNDEDEVEPOPP-----Q 52
DB 1316 NSVEKGSRRILQQQKEVLPALPS-----GSLGDFVLMKGSVN---NPPAAAMSS 1366
QY 53 GPDGCGLPDG-----GDGPPPOPOP-----YDPRLHEVCSVYRDECIYOK 95
DB 1367 GPKKSTPSSLRDIVKEQEKTTSSHPPSPVPTQKAIPQAHQCGAS-----WSR 1418
QY 96 SFAPGSAALSTYPTENLNCKCPGD-----LVEFVSGAOYPHNAVYVGNFQVHLH 146

DB 1419 SASPSQAVSQSSSQ---SKSGDDDLFWGPEVQSTQDTKQGDPPH----- 1461
QY 147 RLEVINSLTDASQGRGRVNV---DLRYKPLS-----SSAVRNALAHGAKERE 195
DB 1462 -LTSQNSWGKNTKTPGK---VNAQSLNRQKSVMSGADRYLSSPVVTQA-SHGKKEAV 1515
QY 196 LSWRNSESFAAWCR 209
DB 1516 TKLTEANGFRDWCCK 1529

RESULT 14

US-11-056-355B-81760
Sequence 81760, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ. ID NOS: 119966
SEQ. ID NO 81760
LENGTH: 1714
TYPE: prt
ORGANISM: Arabidopsis thaliana
NAME/KEY: peptide
LOCATION: (1)..(1714)
OTHER INFORMATION: Ceres Seq. ID no. 12661232
US-11-056-355B-81760

Query Match 5.7%; Score 94.5; DB 7; Length 1714;
Best Local Similarity 23.2%; Pred. No. 45;
Matches 59; Conservative 25; Mismatches 83; Indels 87; Gaps 14;

QY 3 NOVEK-----LTHSYKEVPTADPTGVDRDGPRIQVSYFNSNDEDEVEPOPP-----Q 52
DB 1369 NSVEKGSRRILQQQKEVLPALPS-----GSLGDFVLMKGSVN---NPPAAAMSS 1419
QY 53 GPDGCGLPDG-----GDGPPPOPOP-----YDPRLHEVCSVYRDECIYOK 95
DB 1420 GPKKSTPSSLRDIVKEQEKTTSSHPPSPVPTQKAIPQAHQCGAS-----WSR 1471
QY 96 SFAPGSAALSTYPTENLNCKCPGD-----LVEFVSGAOYPHNAVYVGNFQVHLH 146
DB 1472 SASPSQAVSQSSSQ---SKSGDDDLFWGPEVQSTQDTKQGDPPH----- 1514
QY 147 RLEVINSLTDASQGRGRVNV---DLRYKPLS-----SSAVRNALAHGAKERE 195
DB 1515 -LTSQNSWGKNTKTPGK---VNAQSLNRQKSVMSGADRYLSSPVVTQA-SHGKKEAV 1568
QY 196 LSWRNSESFAAWCR 209
DB 1569 TKLTEANGFRDWCCK 1582

RESULT 15

US-11-056-355B-1197
Sequence 1197, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO: 1197
LENGTH: 219
TYPE: prt
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(219)
OTHER INFORMATION: Ceres Seq. ID no. 12350568
US-11-056-355B-1197

Query Match 5.6%; Score 93.5; DB 7; Length 219;
Best Local Similarity 24.2%; Pred. No. 4.4;
Matches 45; Conservative 14; Mismatches 68; Indels 59; Gaps 7;

Qy	161	GRRGVNDLYRKYKPLSSAVVRNALA-----HVGAKERELSWRNSESFAWCR	209
Db	39	GRRRVAVCCCGWERAGGAAAGAAARCGLVRCRHAGGPRGR--RRRRAGAWRR	95
Qy	210	YGRREFKIGELRIG---KQYRLQIQLSAQSHTLFQSLJEDLIMEKRNQIGRAAV	265
Db	96	QGRRAAAVQBPBGGAEEAORALQAVARPEHLQ-----DGRGDBPRGRRL	146
Qy	266	LQELATLHPAPEPEEGDSNVA-----RTTPPG-----RPPAPS	299
Db	147	-----HGGPALEPGCAAGACGPGGRRRRPRPGPPAAGPGGAGERRVAHAHEPPAPA	200
Qy	300	SEEDG 305	
Db	201	RRDEG 206	

Search completed: December 6, 2006, 21:55:07
Job time : 41 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 6, 2006, 21:41:06; Search time 303 Seconds
(without alignments)
946.386 Million cell updates/sec

Title: US-10-736-227-1

Percent score: 1663
Sequence: 1 MGNGVEKLTLSYKEVPTAD.....PPGRPPAPSSSEEDGEAFAAH 310

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trcembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1663	100.0	310	096KNI_HUMAN	096KNI homo sapien
2	916	55.1	260	04RFD0_TETNG	04RFD0 tetrarodon n
3	859.5	51.7	270	056BP3_BRARE	056BP3 brachydanio
4	642.5	38.6	292	086U22_HUMAN	086U22 homo sapien
5	642.5	38.6	292	087AM5_HUMAN	087AM5 homo sapien
6	642.5	38.6	292	096KNI_HUMAN	096KNI homo sapien
7	637.5	38.3	292	096E50_MOUSE	096E50 mus musculu
8	636.5	38.3	292	099K34_MOUSE	099K34 mus musculu
9	625	37.6	297	03ZCAL_BOVIN	03ZCAL bos tauru
10	599	36.0	260	06PGW5_BRARE	06PGW5 brachydanio
11	581.5	35.0	354	04S116_TETNG	04S116 tetrarodon n
12	269.5	16.2	304	08NAH7_HUMAN	08NAH7 homo sapien
13	250.5	15.1	201	071RD3_HUMAN	071RD3 homo sapien
14	137	8.2	218	04RPF0_TETNG	04RPF0 tetrarodon n
15	136	8.2	164	09UL19_HUMAN	09UL19 homo sapien
16	133.5	8.0	235	08T778_BRARE	08T778 brachydanio
17	131	7.9	228	06P884_XENTR	06P884 xenopus tro
18	129.5	7.8	228	06INW8_XENTR	06INW8 xenopus lae
19	122.5	7.4	158	06PA17_XENTR	06PA17 xenopus lae
20	122	7.3	732	04UBD4_THRAN	04UBD4 theileria a
21	122	7.3	794	08TCS3_HUMAN	08TCS3 homo sapien
22	120	7.2	1219	090710_CHICK	090710 gallus gall
23	118	7.1	162	03V3C3_MOUSE	03V3C3 m 3 days ne
24	118	7.1	162	03V3C3_MOUSE	03V3C3 m 3 days ne
25	117	7.0	162	09NWA9_HUMAN	09NWA9 homo sapien
26	117	7.0	162	09NWA9_HUMAN	09NWA9 homo sapien
27	117	7.0	162	03STI3_HUMAN	03STI3 pongo pygma
28	117	7.0	162	03STI3_HUMAN	03STI3 pongo pygma
29	117	7.0	213	05N1P9_SYNP6	05N1P9 synecococ
30	116.5	7.0	167	05N1P9_SYNP6	05N1P9 synecococ
31	116.5	7.0	167	05D099_MOUSE	05D099 mus musculu

ALIGNMENTS

32	116.5	7.0	776	2	069J16_MOUSE	069J16 mus musculu
33	116.5	7.0	778	2	05RJ15_MOUSE	05RJ15 mus musculu
34	116	7.0	160	1	HRSL3_RAT	HRSL3 rattus norv
35	116	7.0	511	2	04VRH3_OXYSC	04VRH3 oxyuranus s
36	115.5	6.9	231	1	LRAT_RAT	09J161 rattus norv
37	115.5	6.9	231	2	05EAQ3_BRARE	05EAQ3 brachydanio
38	115.5	6.9	561	2	090711_CHICK	090711 gallus gall
39	115	6.9	231	1	LRAT_MOUSE	09J160 mus musculu
40	113	6.8	168	1	HRSL1_HUMAN	09Hdd0 homo sapien
41	113	6.8	168	2	06X7C0_HUMAN	06X7C0 homo sapien
42	113	6.8	1402	2	0709V5_ANOGA	0709V5 anopheles g
43	113	6.8	1963	2	07XFE7_ORYSA	07XFE7 oryza sativ
44	113	6.8	1963	2	094HV2_ORYSA	094HV2 oryza sativ
45	112.5	6.8	725	2	026717_9TRYP	026717 trypanosoma

RESULT 1

AC	096KNI_HUMAN	PRELIMINARY;	PRT;	310 AA.
ID	096KNI1			
DT	01-DEC-2001, integrated into UniProtKB/TrEMBL.			
DT	01-DEC-2001, sequence version 1.			
DE	07-FEB-2006, entry version 15.			
DE	NS22 protein (Breast cancer membrane protein 101).			
GN	Name=NS22; Synonyms=PAM84B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallos D.E.,			
RA	Schneier A., Schein J.E., Jones S.J.W., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
RG	NIH MGC Project;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonCommercial			
CC	License			
DR	EMBL; AJ41849; CAD10629.1; -; mRNA.			
DR	EMBL; BC052957; AAHS2957.1; -; mRNA.			
DR	Ensembl; ENSG00000168672; Homo sapiens.			

DR GO: 0005737; C:cytoplasm; IDA.
 DR GO: 0005886; C:plasma membrane; IDA.
 DR GO: 0005515; F:protein binding; IPI.
 SO SEQUENCE 310 AA; 34474 MW; B587A3F9CB41938 CRC64;

Query Match 100.0%; Score 1663; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1,1e-119;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNQVEKTLTHSYKEVPTADPTGVDKDDGPRIGVSYFISNDDEDEVEPPQPPGPGGGLP 60
 DB 1 MGNQVEKTLTHSYKEVPTADPTGVDKDDGPRIGVSYFISNDDEDEVEPPQPPGPGGGLP 60
 QY 61 DGGGPPPPPOPPYDPRRLHEVCSFYRDECTIQKSFAPGSAALSTYTPENLNKCKRGD 120
 DB 61 DGGGPPPPPOPPYDPRRLHEVCSFYRDECTIQKSFAPGSAALSTYTPENLNKCKRGD 120
 QY 121 LVEFVSQAQYPHMAVYVGNFQVHLHRLLEVINSFLTDSQGRGRVNDLYRYKPLSSSA 180
 DB 121 LVEFVSQAQYPHMAVYVGNFQVHLHRLLEVINSFLTDSQGRGRVNDLYRYKPLSSSA 180
 QY 181 VVRNALAHVGAKEKELSWRNSESFAMCRYGKREPKIGELRIGKQPYRLQIQLSAQRSH 240
 DB 181 VVRNALAHVGAKEKELSWRNSESFAMCRYGKREPKIGELRIGKQPYRLQIQLSAQRSH 240
 QY 241 TLEFQSLLEDLIMEKRNDQIGRAVLQELATHLHRAEEEDSNVARTTPPGRRPAPSS 300
 DB 241 TLEFQSLLEDLIMEKRNDQIGRAVLQELATHLHRAEEEDSNVARTTPPGRRPAPSS 300
 QY 301 EEDGEAVAH 310
 DB 301 EEDGEAVAH 310

RESULT 2

Q4RFD0_TETNG PRELIMINARY; PRT; 260 AA.

AC Q4RFD0_TETNG Integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Chromosome 8 SCAPI5119, whole genome shotgun sequence. (Fragment).
 GN ORFNames=CGTGTG00035376001;
 OS Tetradon nigraviridis (Green puffer).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
 CC Tetraodontidae; Tetraodontidae; Tetraodon.
 CX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jallil O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 Maucel E., Bouneau L., Fischer C., Ozouf-Costez C., Bernot A.,
 Micard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 Desliva C., Salenbadat M., Levy M., Boudet N., Castellano S.,
 Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 Blemont C., Skalli Z., Cateolico L., Poulain J., De Bernardis V.,
 Parra G., Lardier G., Chaplier C., McKernan K.J., McEwan P., Bosak S.,
 Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 Lauder V., Schachter V., Quetier F., Saurin W., Searreli C.,
 Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetradon nigraviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

preliminary data.

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 CC -----
 DR EMBL: CAAB01015119; CAG12902.1; -; Genomic DNA.
 FT NON TER 260
 SO SEQUENCE 260 AA; 29993 MW; 5B93F74B89E5E34 CRC64;

Query Match 55.1%; Score 916; DB 2; Length 260;
 Best Local Similarity 62.5%; Pred. No. 2.9e-62;
 Matches 172; Conservative 42; Mismatches 45; Indels 16; Gaps 4;

QY 1 MGNQVEKTLTHSYKEVPTADPTGVDKDDGPRIGVSYFISNDDEDEVEPPQPPGPGGGLP 59
 DB 1 MGNQVEKTLTHSYKEVPTADPTGVDKDDGPRIGVSYFISNDDEDEVEPPQPPGPGGGLP 51
 QY 60 PDGDDGPPPPPOPPYDPRRLHEVCSFYRDECTIQKSFAPGSAALSTYTPENLNKCKRG 119
 DB 52 LDHFOAMSNHEKRFDDQ-DEBCAHYRECYER-----RSAATHSAESLNKCKRG 105
 QY 120 DLVEFVSQAQYPHMAVYVGNFQVHLHRLLEVINSFLTDSQGRGRVNDLYRYKPLSSS 179
 DB 106 DLVEFVSQAQYPHMAVYVGNFQVHLHRLLEVINSFLTDSQGRGRVNDLYRYKPLSSS 165
 QY 180 AVVRNALAHVGAKEKELSWRNSESFAMCRYGKREPKIGELRIGKQPYRLQIQLSAQRSH 239
 DB 166 VVRNALAHVGAKEKELSWRNSESFAMCRYGKREPKIGELRIGKQPYRLQIQLSAQRSH 225
 QY 240 HTLEFQSLLEDLIMEKRNDQIGRAVLQELATHLH 274
 DB 226 HTLEFQSLLEDLIMEKRNDQIGRAVLQELATHLH 260

RESULT 3

Q56BP3_BRARE PRELIMINARY; PRT; 270 AA.

AC Q56BP3_BRARE Integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Hypothetical protein zgc:110182.
 GN ORFNames=zgc:110182;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mixed tissue.
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
 Brownstein W., Udell T.B., Toshtyuk S., Carninci P., Prange C.,
 Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson R.M.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mixed tissue;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: BC092778; AA92778.1; -, mRNA.
 DR ZFIN: ZDB-GENE-050417-381; zgc:110182.
 KW Hypothetical protein.
 SQ SEQUENCE 270 AA; 3111 MW; 124E589083BCD936 CRC64;

Query Match 51.7%; Score 859.5; DB 2; Length 270;
 Best Local Similarity 59.4%; Pred. No. 6.9e-58;
 Matches 168; Conservative 44; Mismatches 52; Indels 19; Gaps 5;

QY 1 MGNQVEKLTHTLSYKEVPTADPTGVDRDGPRIQVSYIFSNDDDEVPPQPGDGGGL 59
 DB 1 MGNQVEKLTHTLNNELPTADPTGVDRDGPRIQVSYIFSNDDDEVPPQPGDGGGL 47
 QY 60 PDGGDPPPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 119
 DB 48 -ENMDETEVEDVHVDGR-NLECAVYRDEVYERNSRFG--VGLTSLRENLANCKAG 103
 QY 120 DIVERPQVQYPRHMAVYVGNFQVHLHRLLEVINSLPTDASQGRGRVNDLYRKLSS 179
 DB 104 DIVERPQVQYPRHMAVYVGNFQVHLHRLLEVINSLPTDASQGRGRVNDLYRKLSS 163
 QY 180 AVVRNALAHVGAKEKRELKSRNSSESFAAMCRVYGRKBEKIGELRIGQPRLOLSAORS 239
 DB 164 AVVRNALAHVGAKEKRELKSRNSSESFAAMCRVYGRKBEKIGELRIGQPRLOLSAORS 223
 QY 240 HTLEFQSLDLIMEKRRNDQIGRAVLQELATLHLPAPPEEGD 282
 DB 224 HTLEFQSLDLIMEKRRNDQIGRAVLQELATLHLPAPPEEGD 265

RESULT 4
 Q86U22 HUMAN PRELIMINARY; PRT; 292 AA.
 ID Q86U22;
 AC Q86U22;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 12.
 DE Hypothetical protein NSE1.
 GN Name=NSE1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22386297; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grove L.H., Derge J.G.,
 RA Klausner R.D., Collins B., Wagner L., Schmeier C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schmeier C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Ueda T.B., Toehlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Spalding L., Haakenson W., Swearingen S.;
 RT "The sequence of Homo sapiens BAC clone RP11-314E10.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: BC052284; AA52284.1; -, mRNA.
 DR EMBL: AC011897; AA15041.1; -, Genomic DNA.
 DR Ensembl: ENSG00000162981; Homo sapiens.
 KW Hypothetical protein.
 SQ SEQUENCE 292 AA; 32491 MW; 652F11029F517626 CRC64;

Query Match 38.6%; Score 642.5; DB 2; Length 292;
 Best Local Similarity 46.4%; Pred. No. 3.9e-41;
 Matches 137; Conservative 36; Mismatches 87; Indels 35; Gaps 7;

QY 1 MGNQVEKLTHTLSYKEVPTADPTGVDRDGPRIQVSYIFSNDDDEVPPQPGDGGGL 60
 DB 1 MGNQVEKLTHTLNNELPTADPTGVDRDGPRIQVSYIFSNDDDEVPPQPGDGGGL 50
 QY 61 D-EGDPPPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 106
 DB 51 DKGVAAPPCCTPCPSPSRHHHLLHQLVNETQSARGCICFSKXSGCGQADLAV 110
 QY 107 YTPENLANKCKPGDLVEFY-----SQQYPRHMAVYVGNFQVHLHRLLEVINSLPTDAS 159
 DB 111 YAVTALPACERDGLLELMLQPAPEPAPAPAHMAVVGGOIHLHGEIRIDSLYEAG 170
 QY 160 QGRGRVNDLYRKLSSAVVRNALAHVGAKEKRELKSRNSSESFAAMCRVYGRKBEKIG 219
 DB 171 AAVNGRVNSWYRPLVAVLQVONACGHLGKSEECWTNSESFAAMCRVYGRKBEKIG 230
 QY 220 ELRIGKQ-----YRLQIQLSAORSHTLEFQSLDLIMEKRRNDQIGRAVLQELATLHLP 270
 DB 231 EYPAGTQPPQOQYLYKVLHGENKVTARFHSLEDLIREKRIIDASGRRLVQELTA 285

RESULT 5
 Q8TAM5 HUMAN PRELIMINARY; PRT; 292 AA.
 ID Q8TAM5;
 AC Q8TAM5;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 13.
 DE FAM84A protein.
 GN Name=FAM84A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.

NCBI_TaxID=9606;
[1]
NCBIOTIDE SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hunkeler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., USCIN T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
NCBIOTIDE SEQUENCE.
RP TISSUE=Brain;
RC NIH MGC Project;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
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CC
EMBL: BC026346; AAH26346.1; -; mRNA.
DR Ensembl; ENSG00000162981; Homo sapiens.
DR SEQUENCE 292 AA; 32532 MW; EA3F807C1F469F56 CRC64;
Query Match 38.6%; Score 642.5; DB 2; Length 292;
Best Local Similarity 46.4%; Pred. No. 3.9e-41;
Matches 137; Conservative 36; Mismatches 87; Indels 35; Gaps 7;
QY 1 MGNQVEKTLHSYKVEPTADPTGVDPRIGSYFNSNDEVEPQPPQGGSLP 60
DB 1 MGNQIDRITHLYSELPTGDSGIEKDE-LRVGVAFFSDDEEDL-----DERQOP 50
QY 61 D--GGDPPPPQPPQPPQPPRLH-----EVECSYFYRDECTYOK-SFAPGSAALST 106
DB 51 DKGFKAPPGCTPCBPESRHHHLLHQLVLTETQPSAFRQECIFSKVSGGPGQADLSV 110
QY 107 YTPENLNKCKRPGDLVEFV-----SQOYPMHVVYGNFQVHLRLVINSFLTDAS 159
DB 111 YAVTALPALCEPGLLELMTQLQHAPEPAPAPHMAVYGGQIITHHGEIRQDSLYBAG 170
QY 160 CGRRGRVYNDLYRKPSSSAVYRNALAHVAKRELSESRNSESFAAMCRKGRKFKIG 219
DB 171 AANVGRVYNSWYRRPVLAEVLVQNAQCHLGLKSEECWTNSESFAAMCRKGRKFKIG 230
QY 220 ELRIGKOP-----YRLQIQLSAQRSHLTFOSLEDLIMEKRNDQIGRAVLOELA 270
DB 231 EVPAQTQPPQOQYTLKVLGKNTATAFHSLEDLIREKRNDQIGRAVLOELA 285
RESULT 6
Q96KN4 HUMAN PRELIMINARY: PRT; 292 AA.
AC Q96KN4; 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE NSE1 protein.
GN Name=NSE1;
OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
CC Homo.
NCBI_TaxID=9606;
[1]
NCBIOTIDE SEQUENCE.
RP Hughes P.J., Stanway G.;
RA Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
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CC
EMBL: AJ417080; CAP10038.1; -; mRNA.
DR Ensembl; ENSG00000162981; Homo sapiens.
DR SEQUENCE 292 AA; 32482 MW; BA5580ADE3FE345A CRC64;
Query Match 38.6%; Score 642.5; DB 2; Length 292;
Best Local Similarity 46.4%; Pred. No. 3.9e-41;
Matches 137; Conservative 36; Mismatches 87; Indels 35; Gaps 7;
QY 1 MGNQVEKTLHSYKVEPTADPTGVDPRIGSYFNSNDEVEPQPPQGGSLP 60
DB 1 MGNQIDRITHLYSELPTGDSGIEKDE-LRVGVAFFSDDEEDL-----DERQOP 50
QY 61 D--GGDPPPPQPPQPPQPPRLH-----EVECSYFYRDECTYOK-SFAPGSAALST 106
DB 51 DKGFKAPPGCTPCBPESRHHHLLHQLVLTETQPSAFRQECIFSKVSGGPGQADLSV 110
QY 107 YTPENLNKCKRPGDLVEFV-----SQOYPMHVVYGNFQVHLRLVINSFLTDAS 159
DB 111 YAVTALPALCEPGLLELMTQLQHAPEPAPAPHMAVYGGQIITHHGEIRQDSLYBAG 170
QY 160 CGRRGRVYNDLYRKPSSSAVYRNALAHVAKRELSESRNSESFAAMCRKGRKFKIG 219
DB 171 AANVGRVYNSWYRRPVLAEVLVQNAQCHLGLKSEECWTNSESFAAMCRKGRKFKIG 230
QY 220 ELRIGKOP-----YRLQIQLSAQRSHLTFOSLEDLIMEKRNDQIGRAVLOELA 270
DB 231 EVPAQTQPPQOQYTLKVLGKNTATAFHSLEDLIREKRNDQIGRAVLOELA 285
RESULT 7
Q9D650 MOUSE PRELIMINARY: PRT; 292 AA.
AC Q9D650; 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE 10 days neonate skin cDNA, RIKEN full-length enriched library,
DE clone:4731402F03 product:NSE1 PROTEIN homolog.
GN Name=AW125753;
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
NCBIOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
[2]
NCBIOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Skin;
RC PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Allen J.E., Allen J.E., Allen J.E., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Auraliyya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Batsakis T., Bono H., Chalk A.M.,

RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dairymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Guerninich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Keiso J., Kikunaga H.,
RA Kitano H., Kohli A., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motegut-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Oriando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempé C.A., Seno S., Sessa L., Sheng Y.,
RA Shilbata Y., Shimada K., Shima D., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Telchmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K.,
RA Yamashiki H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
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RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
[27]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kikunaga T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
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RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
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RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kikunaga T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
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RC STRAIN=C57BL/6J; TISSUE=Skin;
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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
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RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
[30]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kikunaga T., Tashiro H., Itoh M.,
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RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
[32]
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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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RA Konno H., Akiyama J., Nishi K., Kikunaga T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA)

Best Local Similarity 56.9%; Pred. No. 2e-36;
Matches 119; Conservative 21; Mismatches 42; Indels 27; Gaps 5;

QY 1 MGNQVEKTLTHLSYKVEPTADPTGVDRDDGPRIGVSYIFSNDEDEVEPOPPGPDGGLP 60
Db 1 MGNQADLHLSLVAEPTVPNGVDADGSRIGVSYIFSND-DEEPE----- 47

QY 61 DGGDPPPOPPQPYDPPLHVECSVFYRDECITYOKSAFGSAALSTTPENTLNKCKRPGD 120
Db 48 ECGGASDSNOBEKLFDRDEDECAVFRDDCVYER--RARRASLEVYSPEMLNRCRAGD 105

QY 121 LVEVSGAQQYPHAAVYVGNFQVHLHLEVINSLFTDASQGRGRGVVNDLYRYKPLSSA 180
Db 106 L-----YPHAAVYVGDFOVHLHRAEVKNSFLTDASGRGRGVVNDLYRYKPLGFEV 157

QY 181 VERNALAHVGAKEKRELSWRNSESFAAMCR 209
Db 158 VVONAMEQVGLKODELSMRNSES-----CR 182

RESULT 12
Q8NAH7_HUMAN PRELIMINARY; PRT; 354 AA.

AC ORNAH7, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-MAR-2006, entry version 12.
DE CDNA FLJ35335 f18, clone PROSTR2015287.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Ohtsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Magatsuma M., Shizatori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda T., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki K.,
RA Ninomiya K., Ishibashi T., Yamashita K., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirooka S., Chida Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Ariita M., Imose N.,
RA Muraashino K., Yuuki H., Oshima A., Sasaki N., Aotsuba S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Komiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Omori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs";
RL Nat. Genet. 36:40-45(2004).
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CC
CC EMBL; AK092654; BAC03938.1; -; mRNA.

DR Ensemble1; ENSG00000162981; Homo sapiens.
SQ SEQUENCE 354 AA; 37751 MW; DF510D1FE9F93CID CRC64;
SO Query Match 16.2%; Score 269.5; DB 2; Length 354;
Best Local Similarity 32.8%; Pred. No. 2.6e-12;
Matches 76; Conservative 25; Mismatches 80; Indels 51; Gaps 10;

QY 1 MGNQVEKTLTHLSYKVEPTADPTGVDRDDGPRIGVSYIFSNDEDEVEPOPPGPDGGLP 60
Db 1 MGNQADLHLSLVAEPTVPNGVDADGSRIGVSYIFSND-DEEPE----- 47

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Db 51 DKFGVKAAPGCTPCPEPSRHHHLHLQVLNLFOTFSAFRGOECIFSVSGGPGCADLSV 110

QY 107 YTPENLNKCKRPGDLVEFV-----SOAQYPHAAVYVGNFQVHLHLEVINSLFTDAS 159
Db 111 YAVTALPALCEPGLLELMLQPAPEPPAPAPHAASRRR-SAGRTTBASPPGAAIASGS 169

QY 160 QGRGRGVVNDLYRYKPLSSAVVARNALAHVGAKEKRELSWRNSESFAAM 207
Db 170 SRREGRC---RQASPRSSSTISR-----CTWERTRTSTPGFTAM 206

RESULT 13
Q71RD3_HUMAN PRELIMINARY; PRT; 201 AA.

AC Q71RD3, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 05-JUL-2004, entry version 1.
DT 07-FEB-2006, sequence version 5.
DE P11517.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
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CC distributed under the Creative Commons Attribution-NonDerivs license
CC
CC EMBL; AF370404; AA015240.1; -; mRNA.
SO SEQUENCE 201 AA; 22213 MW; 74297F23D71EB39F CRC64;

Query Match 15.1%; Score 250.5; DB 2; Length 201;
Best Local Similarity 51.5%; Pred. No. 3.6e-11;
Matches 53; Conservative 10; Mismatches 35; Indels 5; Gaps 2;

QY 157 DASQGRGRGVVNDLYRYKPLSSAVVARNALAHVGAKEKRELSWRNSESFAAMCRGKREFK 216
Db 75 EAGANVGRVNVSWYRRPLVAELVQACHTLGKSEICMTWSESPFAAMCRGKREFK 134

QY 217 IGGELRIKQPYRQIQQLSA-----QSRHTLEFQSLIEDIMEKR 255
Db 135 AGGEVPAFLADPAALVLSGAGRGQGPFR-OFHSLDELIREKR 176

RESULT 14
Q4RPT7_TETNG PRELIMINARY; PRT; 218 AA.

AC Q4RPT7, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 4.
DT 19-JUL-2005, entry version 1.
DT 07-FEB-2006, entry version 1.
DE Chromosome 1 SCAP15008, whole genome shotgun sequence.
GN ORFNames=GSTENG00031172001.
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Oy	158	ASGRRGRVNDL-YRYKPLSSAVRNALAHGAKER-ELSMRNSSEFPAACRYGKREF	215
Db	68	VVGCCYRVNNSLDHEYOPRPVEVVISSAKEMVGOIKMKYSIVSRNCEHFTQLRYGKGRG	127
Oy	216	K 216	
Db	128	K 128	

Search completed: December 6, 2006, 21:49:21
 Job time : 307 secs

TITLE OF INVENTION: RETINOID INDUCED GENE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,303
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: ALRGN.062A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-808-303-12

Query Match 8.5%; Score 141; DB 1; Length 164;
Best Local Similarity 32.2%; Pred. No. 1.7e-06;
Matches 39; Conservative 21; Mismatches 39; Indels 22; Gaps 5;

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DB 9 KPGDLLE-IFRLGIEHMLYIGGYVHLAPPEYPCAGSSVSFVLSNBAEVKRGRLD 67

QY 165 -----RVVNDL-YRYKPLSSSAVVNNAALAHVGAKER-ELSMRNSESFAWCRYGKREF 215
DB 68 VVGCCCVRVNNSLDHEQPRPVEVLIISAKEMVQKMKYSIVSRNCEHFVAQLRYGKSR 127

QY 216 K 216
DB 128 K 128

RESULT 3
US-08-996-533-12
Sequence 12, Application US/08996533
Patent No. 6294657
GENERAL INFORMATION:
APPLICANT: Nagpal, Sunil
APPLICANT: Disepio, Daniel
APPLICANT: Chandraratna, Roshantha
TITLE OF INVENTION: RETINOID INDUCED GENE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,533
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,303
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: ALRGN.062A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-996-533-12

Query Match 8.5%; Score 141; DB 2; Length 164;
Best Local Similarity 32.2%; Pred. No. 1.7e-06;
Matches 39; Conservative 21; Mismatches 39; Indels 22; Gaps 5;

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QY 165 -----RVVNDL-YRYKPLSSSAVVNNAALAHVGAKER-ELSMRNSESFAWCRYGKREF 215
DB 68 VVGCCCVRVNNSLDHEQPRPVEVLIISAKEMVQKMKYSIVSRNCEHFVAQLRYGKSR 127

QY 216 K 216
DB 128 K 128

RESULT 4
US-08-808-303-8
Sequence 8, Application US/08808303
Patent No. 5776687
GENERAL INFORMATION:
APPLICANT: Nagpal, Sunil
APPLICANT: Disepio, Daniel
APPLICANT: Chandraratna, Roshantha
TITLE OF INVENTION: RETINOID INDUCED GENE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,303
FILING DATE:
CLASSIFICATION: 435

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 6, 2006, 21:49:36 ; Search time 52 Seconds
(without alignments)
521.817 Million cell updates/sec

Title: US-10-736-227-1

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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /EMC_Celerra_SIDS3/pcodata/2/1aa/6_COMB.pep.*
3: /EMC_Celerra_SIDS3/pcodata/2/1aa/7_COMB.pep.*
4: /EMC_Celerra_SIDS3/pcodata/2/1aa/H_COMB.pep.*
5: /EMC_Celerra_SIDS3/pcodata/2/1aa/PCTUS_COMB.pep.*
6: /EMC_Celerra_SIDS3/pcodata/2/1aa/RE_COMB.pep.*
7: /EMC_Celerra_SIDS3/pcodata/2/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	141	8.5	164	1 US-08-808-303-12	Sequence 12, App1
3	141	8.5	164	2 US-08-996-533-12	Sequence 12, App1
4	136	8.2	164	1 US-08-808-303-8	Sequence 8, App1
5	136	8.2	164	2 US-08-996-533-8	Sequence 8, App1
6	136	8.2	164	2 US-08-801-742-1	Sequence 1, App1
7	122	7.3	703	2 US-10-116-326-6	Sequence 6, App1
8	122	7.3	703	2 US-10-803-377-6	Sequence 6, App1
9	122	7.3	762	2 US-10-116-326-4	Sequence 4, App1
10	122	7.3	762	2 US-10-803-277-4	Sequence 4, App1
11	122	7.3	778	2 US-10-116-326-2	Sequence 2, App1
12	122	7.3	778	2 US-10-003-690-2	Sequence 2, App1
13	122	7.3	778	2 US-10-803-277-2	Sequence 2, App1
14	116	7.0	160	2 US-08-801-742-4	Sequence 4, App1
15	114	6.9	162	2 US-08-801-742-3	Sequence 3, App1
16	113	6.8	522	2 US-10-104-047-3665	Sequence 3665, App1
17	109	6.6	603	2 US-09-930-181-17	Sequence 17, App1
18	109	6.6	614	2 US-10-283-247-9	Sequence 9, App1
19	109	6.6	614	2 US-10-283-247-10	Sequence 10, App1
20	109	6.6	636	2 US-10-283-247-5	Sequence 5, App1
21	109	6.6	674	2 US-10-283-247-2	Sequence 2, App1
22	109	6.6	674	2 US-10-283-247-7	Sequence 7, App1
23	109	6.6	674	2 US-10-283-247-8	Sequence 8, App1
24	103.5	6.2	572	2 US-09-543-681A-7137	Sequence 7137, App1
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29	101.5	6.1	328	2 US-09-370-270-1	Sequence 1, App1
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ALIGNMENTS

```

RESULT 1
US-10-104-047-3151
Sequence 3151, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104, 047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3151
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3151

Query Match 16.2%; Score 269.5; DB 2; Length 354;
Best Local Similarity 32.8%; Pred. No. 2.2e-19; Indels 51; Gaps 10;
Matches 76; Conservative 25; Mismatches 80;

QY 1 MGNQVEKTLTHLSYKEVPTADPTGVDRDDGPRIGSVYIFSNDDVDVEPQPPGGGLP 60
DB 1 MGNQDLRITHTLVNSELPTGDPGIEKDE-LRVGVAVFFSDDEDL-----DERGQF 50
QY 61 D--GGDPPPPQPPYDPRLLH-----EVEGVPFRDCTIYK-SFAPGSALST 106
DB 51 DKFGVAPPCCTCPSPSRHHHLLHQLVLTNTPSFAFGQBCIFSKVGGPGGALSLV 110
QY 107 YTEPNLNNCKPDPDIVEFV-----SQAQYPMNAVYVNGFQVHLRLVINSFLTDAS 159
DB 111 YAVTALPACEDPDLLEMLQAPAPPPAPAPAPASARK-SAGRTTRASPPGAAALASGS 169
QY 160 QGRGRGVNDLVYRKPLSSAVVNNALAHGAKEREISWNSSES---FAAW 207
DB 170 SRREGRC---RQARSPPRSSSTISR-----CTWERTSTPPTGFTAW 206

RESULT 2
US-08-808-303-12
Sequence 12, Application US/08808303
Patent No. 576687
GENERAL INFORMATION:
APPLICANT: Nagpal, Sunil
APPLICANT: Disepio, Daniel
APPLICANT: Chandraratna, Roshantha

```


Db 737 GL 738

RESULT 9
formin - mouse
S11515

C:Species: Mus musculus (house mouse)

C>Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S11515

R:Moynick, R.P.; as, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.

Nature 346, 850, 1990

A:Title: 'Formin' proteins deduced from the alternative transcripts of the limb deform

A:Reference: 'Formin' S11515; PMID:90363291; PMID:2392150

A:Accession: S11515

A:Molecule: mRNA

A:Residues: 1-1468 <MO>

A:Cross-references: UNIPROT:Q05860; UNIPARC:UPI0000027927; EMBL:X53599; NID:G52877; PIDN:

Query Match 5.8%; Score 96.5; DB 2; Length 1468;

Best Local Similarity 37.1%; Pred. No. 18;

Matches 23; Conservative 2; Mismatches 24; Indels 13; Gaps 1;

Db 17 PPADPTGVDRDGPRIQVYIFSNDDVEYPPQPGGGLPDGSGPPPPQPPQPP 76

916 PPPPPPPVPPSDGP-----PPPPPPPLPVYALPNSGGPPPPPPPPPP 962

Qy 77 RL 78

Db 963 GL 964

RESULT 10

A:Accession: A53327

hypothetical protein BMEI0603 (imported) - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: A53327

R:DelVecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

M.; Masur, M.; Goldsman, E.; Selkov, E.; Elker, P.H.; Hagluer, S.; O'Callaghan, D.; Letess,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: A53327

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-189 <KUR>

A:Cross-references: UNIPROT:Q8Y142; UNIPARC:UPI0000057D45; GB:AE008917; PIDN:ALM51784.1;

A:Experimental source: strain 16M

A:Gene: BMEI0603

A:Map position: 1

Query Match 5.7%; Score 95.5; DB 2; Length 189;

Best Local Similarity 25.8%; Pred. No. 1.4;

Matches 47; Conservative 26; Mismatches 56; Indels 53; Gaps 10;

Db 166 VVNDLRYRPLSSA---VVRNALAH-----VGAKEKELSWRNSESFA 205

1 MVDLRLVILQGEALRGVIRKVLAEAKAGLPGNHFFITPLTGAQVIRISRLKEXP 60

Qy 206 A-----WCRYKRE-FKIGELRLGKQRYRLOLSAOR-----SHLLEFQSL 247

Db 61 EGMWTLVQHOFMFMHVTDLFEVGL--LSFGDIPKLTIPPSAIRGVDPSVNELEF--- 115

Qy 248 EDLIMEKRRNDQGRAVLOELATHLPAPEEGDSNVART--TPPGRRPAP--SEED 304

Db 116 DVAVLDPASDNDGNSPIEFMA-----PEKADRPKAKTRKPAAGKESASTDSEOD 168

Qy 305 GE 306

Db 169 GE 170

RESULT 11

E29149

proline-rich protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004

C:Accession: E29149

R:Clements, S.; Menasho, H.; Carlson, D.M.

J. Biol. Chem. 260, 13471-13477, 1985

A:Title: Novel multigene families encoding highly repetitive peptide sequences. Sequence

A:Reference number: A92501; PMID:86033799; PMID:3840480

A:Contents: Clone pUMR125

A:Accession: E29149

A:Molecule type: mRNA

A:Residues: 1-301 <CL>

A:Cross-references: UNIPROT:Q62105; UNIPARC:UPI00000286D2; GB:M11897; NID:G200540; PIDN:

C:Superfamily: Proline-rich peptide P-8

Query Match 5.7%; Score 95.5; DB 2; Length 301;

Best Local Similarity 34.0%; Pred. No. 2.6;

Matches 32; Conservative 6; Mismatches 27; Indels 29; Gaps 6;

Qy 1 MGNQVEXLTHLSYKE---VPTADPTGVDRDGPRIQVYIFSNDDVEY-----PO--- 48

Db 35 MGEQSGYGHHRKPPPGMPPRPSSGENDGSDG-----SEEDVNGGERPPQHP 87

Qy 49 -----PPPGGPGGGLPDGSD--GPPPPQPP 73

Db 88 HSGHHHGPPPG--DAQPPRPNGOQPPPPGPP 120

RESULT 12

C87719

protein R119.6 (imported) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C87719

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; PMID:99069613; PMID:9851916

A:Note: see websites genome.usci.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_e

A:Note: published extra appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: C87719

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-549 <STO>

A:Cross-references: UNIPROT:Q61707; UNIPARC:UPI00000790D5; GB:chr_I; PIDN:AA16427.1; P:

C:Genetics:

A:Gene: R119.6

A:Map position: 1

Query Match 5.7%; Score 95.5; DB 2; Length 549;

Best Local Similarity 20.6%; Pred. No. 5.8;

Matches 72; Conservative 37; Mismatches 116; Indels 125; Gaps 15;

Qy 18 TADPTGVDRDGPRIQVYIFSNDDVEYPPQ----- 50

Db 210 TASVGVNPPPG-----YVFNNGRTPGPQPPPPQOQOQPPLEMRQIPNPNOIPQM 263

Qy 51 -----PQPPGGGLPDGSDP-----PPPOPO-----PY 74

Db 264 VGGGHMVSVGARPMIRKMP--GGSPGGLQCPVAGPMQHMVQNMPPPPPOIOQONRA 322

Qy 75 DPLHEVECSVFYRDECTYKSFAPSAALSTYPENILNK-----CK--PGLVEFV 125

Db 323 PVEWEVEENLQPTAATATATROYRPGSLKSTIKEDDEVILNRTKRMSSGSVEREALVAI 382

Qy 126 SOAQYRNAVYVGNQVNVHLHLE---VINSFLTASQGRGRVNVNDLYRYKPLSSAVV 182

Db 383 SDVESHLELITLMAGVAENRVESLRIPENVALVDVYKRLRFLEDDR----- 432

Qy 183 RNALAHVGAKEKELSWRNSESFAWCRVYKGEFKIGELRIGKQRYRLOLSAORSHTL 242

```

Db      243 AELFELVGPITLHNMKMAERGRFFELIEFCENGEPLTMVPPVVSQSDILHRL---- 299
Qy      152 NSFPLDASQGRGRGVNDLYRYKPLSSSAVVRNALAHVAKEREISMRN-----SE 202
Db      300 --YICVRKAGCGOQVTKDKY-----MKNLCTEANDDLAE 331
Qy      203 SFAMCRVGRKREPKTGGELRTGKQPRLOIQ--SAQRSHTEFQSLIEDLIMEKRNDQIG 261
Db      332 SSAA-----GYQLRKAYORHLMLSECRTEGRNDEDEVAFADKKRQRKREPAG 380
Qy      262 RAAVLOELATHLHPAREEGDSNVARTPPGRRPA 297
Db      381 NAAAAAANAAGGCGDKSGHGAFGSSGAPPPGPRGA 416

```

RESULT 6

H71332
hypothetical protein TP0369 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: H71332

R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rean, J.; Kralak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Ueberback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:965876

A:Accession: H71332

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-516 <COL>

A:Cross-references: UNIPROT:083384; UNIPARC:UPI00001396D0; GB:AE001216; GB:AE000520; NIT

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0369

```

Query Match      5.9%; Score 97.5; DB 2; Length 516;
Best Local Similarity 24.1%; Pred. No. 3.6; Mismatches 103; Indels 101; Gaps 17;
Matches 73; Conservative 26;

Qy      47 POPPGPGGGLPDGDDGPPPOPPYPRRLHEVSCSYFRDECIYOKSFAPGSAALST 106
Db      138 PEPPEPSP-SAGRPKQRAVPSPSPASPEPRAEVQAE-----PEPRADS- 181
Qy      107 YTPENLNKCKGPDLYEVSQA-----QYP-HNAVYVGNFQV-----VILHKL 148
Db      182 --PRAVPEEPPEDEVPVRSRAVOLAVGOKLEVLTYGEGW-VYVGHTAQPGLRYHQKX 238
Qy      149 EVINSPLTASQGRGRGVNDLYRYKPLSSSAVVRNALAHVAKEREISMRNSEFAMC 208
Db      199 EESHSLFTLSAE-REGDFVL-AFSYDFVPRGDFVSALAVKVPKKE----- 283
Qy      21 NGKREFKTGGELRTGKQPRLOIQ-----QLSAQRSHTEFQSLIEDLIMEKRND 258
Db      28 NGKREFKTGGELRTGKQPRLOIQ-----QLSAQRSHTEFQSLIEDLIMEKRND 258
Qy      259 QI--AAVLOELATHL-HPAAREEGDSNVART--TPP-----GRPPASSEE 302
Db      322 EAGTSG-SQRAAAHTGAPVNDQDTDTVAVAKAQHGTPRPDEKDRPTVGRDPVPSDAV 380
Qy      303 EDG 305
Db      381 AAG 383

```

RESULT 7

SS5345
protein-tyrosine-phosphatase (EC 3.1.3.48) PTP-PEST - mouse.

C:Species: Mus musculus (house mouse)

C:Date: 10-Oct-1995 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004

C:Accession: S55345; S54261; I48666

R:Charest, A.; Wagner, J.; Shen, S.H.; Tremblay, M.L.

```

Biochem. J. 308, 425-432, 1995
A:Title: Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyrosine
A:Reference number: I48666; MUID:95289971; PMID:7772023
A:Accession: S55345
A:Molecule type: DNA
A:Residues: 1-775 <CHA>
A:Cross-references: UNIPROT:P35811; UNIPARC:UPI000017598B; EMBL:X86781; NID:9804997; PI
submitted to the EMBL Data Library, May 1995
R:Charest, A.; Wagner, J.; Shen, S.H.; Tremblay, M.L.
A:Description: Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein ty
A:Reference number: S54261
A:Accession: S54261
A:Molecule type: DNA
A:Residues: 1-127, 'M', 129-309, 'R', 311-775 <CHW>
A:Cross-references: UNIPARC:UPI000028ARD; EMBL:X86781; NID:9804997; PID:CAA60477.1; P
A:Experimental source: strain BALB/c
C:Genetics:
A:Map position: 5A3-B
C:Superfamily: protein-tyrosine phosphatase, non-receptor type 12; protein-tyrosine-pho
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata
F:58-282/Domin: protein-tyrosine-phosphatase homology <PTP>
F:231/Active site: Cys (phosphocysteine intermediate) #status predicted
F:237/Binding site: substrate phosphate (Arg) #status predicted

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Query Match      5.9%; Score 97.5; DB 2; Length 775;
Best Local Similarity 18.7%; Pred. No. 6.3;
Matches 53; Conservative 35; Mismatches 109; Indels 87; Gaps 9;

```

```

Qy      28 DCPRIGVSYFSDNDEVEPPPPGPGGGLPDGDPG---PPQPPYPRRLHEVEC 83
Db      311 DQNEITGTWVSSISEKQDSDPPKPRTRSCLVEDAKKEILLQPEPHVPEILTPSP 370
Qy      84 SYFYDECIYOKSFAPGSAALSTYTPENLNKCKGPDLYEVSQAQYPPHNAVYVGNFQV 143
Db      371 SAFPVTYTWQDS-----DRHPKPYLHNASP----- 397
Qy      144 HLHRLVINSPLTASQGRGRGVNDLYRYKPLSSSAVVRNALAHVAK-EREISMRNSE 202
Db      398 EGHPPADLNNSYKSAQDWQKS-----ESAIEHIDKLERLTSF----- 435
Qy      203 SFAMCRVGRKREPKTGGELRTGKQPRLOIQSLAQRSHTEFQSLIEDLIMEKR----- 255
Db      436 -----EIK--KVPLOEGPKSPFDGNTLNNGHAIKIKSASSSVVDRTSKQELS 481
Qy      256 -----RNDIGRAAVLOELATHLHPAREEGDSNVARTPPGRRP 295
Db      482 AGALKVDVDSQNSCADCSAAHSHRAESSEESQNSHTPP--RP 523

```

RESULT 8

S24407
formin isoform IV - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S24407

R:Jackson-Grusby, L.; Kuo, A.; Leder, P.

Genes Dev. 6, 29-37, 1992

A:Title: A variant limb deformity transcript expressed in the embryonic mouse limb defi

A:Reference number: S24407; MUID:92112033; PMID:1339380

A:Accession: S24407

A:Molecule type: mRNA

A:Residues: 1-1206 <JAC>

A:Cross-references: UNIPROT:Q05859; UNIPARC:UPI0000027920; EMBL:X62379; NID:G51552; PID

```

Query Match      5.8%; Score 96.5; DB 2; Length 1206;
Best Local Similarity 37.1%; Pred. No. 14;
Matches 23; Conservative 2; Mismatches 24; Indels 13; Gaps 1;

Qy      17 PTAADPTGVDNDGPRIGVSYFSDNDEVEPPPPGPGGGLPDGDDGPPPOPPYPR 76
Db      690 PPPPPPPPPSPDP-----PPPPPPPPPLPVLLPLNSGCGPPPPPPPPPP 736
Qy      77 RL 78

```

RESULT 15

US-08-801-742-3

: Sequence 3, Application US/08801742
: Patent No. 6359123

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: A NOVEL H-REV107-LIKE

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,742

FILING DATE: Filed Herewith

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0200 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: Genbank

CLONE: 1054752

08-801-742-3

Query Match 6.9%; Score 114; DB 2; length 162;

Test Local Similarity 33.6%; Pred. No. 0.0011;

Matches 39; Conservative 17; Mismatches 38; Indels 22; Gaps 6;

QY 117 KPGDLVEFVSQAOYPMNAVYVGNFOVHL-HRLEV-----INSFLLTDS-----159

DB 9 KRDDLIE-IFRPYRMAIYVGDGYVHLAPSEVAGAGASVMSALTDKAIYKKELLYD 67

QY 160 -QGRRGVVNDLY--RYKPLSSAVVNNALAHVGAKE-RELSWRNSESFAACRYG 211

DB 68 VAGSDKYQVNNKDDKYSPLPCTKIQRABELVGEVLYKLTSENCEHFVNEELRYG 123

Search completed: December 6, 2006, 21:51:07

Job time : 54 secs

```

Query Match 8.2%; Score 136; DB 2; Length 164;
Best Local Similarity 32.2%; Pred. No. 5.6e-06;
Matches 39; Conservative 15; Mismatches 45; Indels 22; Gaps 4;

QY 117 KEGDLVEFVSOAQPMAVYVGNFOVHL-----HRLEVINSEFLTD 157
DB 9 KPGDLIE-IFRLGIEHMAIYIGDGYVHILAPSEYVGCAGSSVSVLSNAGVKKRLELD 67
QY 158 ASOGRGQVNDL-YRYEPLSSAVRNALAHGAKER-ELSRNSESFAAMCRYGKREF 215
DB 68 VVGCCYTRVNSLDEHOPRVEVLISSAKENVGQMKRYSIVSRNCEHFVTLQRYGKSR 127
QY 216 K 216
DB 128 K 128

RE:ULT 7
US-10-116-326-6
; Sequence 6, Application US/10116326
; Patent No. 677545
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Machut, Brian
TITLE OF INVENTION: No. 677545e1 Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0332-USA
CURRENT APPLICATION NUMBER: US/10/116.326
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,036
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 703
TYPE: PRT
ORGANISM: homo sapiens
US-10-116-326-6

Query Match 7.3%; Score 122; DB 2; Length 703;
Best Local Similarity 21.6%; Pred. No. 0.0014;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;

QY 50 PPGGPGGGGLPDGSDGPPPO-----POPYD----- 76
DB 404 PSRGGPRGG---AGEOPPPPSARSTPLPGPGSPRSSGCTPLHSPLHTPRASPTGTPTT 460
QY 77 -----RLHEVEGCVFYRDECIYKSPFAGSAALSTYPERINLCKCKPD 120
DB 461 PPPSPGGGVGAAMRSLNLSIRNSFLSPRRHRKMOVTLBEMSSLTPELAKS- 519
QY 121 LVEFVSOAQYPMVAVYVGNFOVHLRLLEVINSEFLTDASQGRGRVNDLYRKPFLSSGA 180
DB 520 -----WFGNF--ISLDKKEQFLVLKD-----KFLSS-- 544
QY 181 VVRNALAHGAKERELSMR--NSESFAAMCRYGKREFLIGELRIGKQPYRLOTLSAQR 238
DB 545 -IKADIVHAFSLPSLSHVSLSOTSPRA-----EYASGSPSVFQKRVFQVDISSSE 596
QY 239 S-----HTLEFOSLIEDLIMKRRNDQIGRAVLOELATHLHPAEPEEGD- 282
DB 597 GPEPSRRDOSGGGIVSVFTLISG---PSRRKRVETIQAQLSLTHDQPSVQALADE 653
QY 283 SNVART-----TPPGRP-PAPSSEEDG 305
DB 654 KNGAOTRPAQAPPRSLQPPGRDPPELSSSPRRG 687

RESULT 8
US-10-803-277-6
; Sequence 6, Application US/10803277
; Patent No. 6919192
GENERAL INFORMATION:

```

```

; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Machur, Brian
; APPLICANT: Fridtle, Carl Johan
; TITLE OF INVENTION: No. 6919192el Human Kinases
; FILE REFERENCE: LEX-0332-US#
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 703
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-803-277-6

```

```

Query Match      7.3%; Score 122; DB 2; Length 703;
Best Local Similarity 21.6%; Pred. No. 0.0014;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;

QY PPGGPDGGGLPDGGDPPPPQ-----PQYPDP----- 76
Db PSRGRPCGG---AGEQPSPASSTPLPPGPSPRSSGGTPLHSLPHTRAPSGTGT 460
QY 77 -----RLHEVECSVYRDECTIYOKSFAPGSALSTYPTENLKKCPGD 120
Db PPSPGGGVGAGAMRSRLNSIRNSFLGSDPRFHRRKQVPPTAEBSLSLTPESSBELAKRS- 519
QY 121 LVEFVGQAQPHAAVVVGNFOVHLHRELVINSFLTDAQGCRGRVNDLYRKXPLSSSA 180
Db 520 -----WFGNF--ISLDKEQITPLVLD-----KPLSS-- 544
QY 181 VVNALAHVAKERELESMWR--NSESPACMCRGYKEEFGIGELRICOPRYLOIOLSAQR 238
Db 545 -IADIVHAFLSTPSLSHSVLSTSPRA-----EYKASGGPSVFQKVRFOVDISSSE 596
QY 239 S-----HTLFQSLEDLLMEKRNDQIGRAAVLOELATHLHAPPEECG- 282
Db 597 GPSPSRDDGGGGGGGIYSTFTLISG---PSRRPFKVETIQQLSLTHDQPSVALADE 653
QY 283 SNVART-----TPPPGRP-PAPSSEEDG 305
Db 654 KNGAQTRPAGAAPPRTSLQPPGRPPDELSPSRPG 687

RESULT 9
US-10-116-326-4
Sequence 4, Application US/10116326
Patent No. 6777545
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Machur, Brian
APPLICANT: Fridtle, Carl Johan
TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the Sa
FILE REFERENCE: LEX-0332-USA
CURRENT APPLICATION NUMBER: US/10/116,326
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,036
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 762
TYPE: PRT
ORGANISM: homo sapiens
US-10-116-326-4

Query Match      7.3%; Score 122; DB 2; Length 762;
Best Local Similarity 21.6%; Pred. No. 0.0016;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;
```


LENGTH: 778
TYPE: PRT
ORGANISM: Homo sapiens
US-10-003-690-2

Query Match 7.3%; Score 122; DB 2; Length 778;
Best Local Similarity 21.6%; Pred. No. 0.0017;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;

50 PPGPGGGLPDDGDDPPPO-----PPYDP----- 76
479 PSRCPGCGG---AGEOPPPSARSTPLPGPGSSSGTPLHSPHTPRASPTGTPTT 535
77 -----RLHEVCGSVFYRDECIYOKSFAPGSAALSTYTPENLTKCKPGD 120
536 PPSPGGCGVGAAMRSRLNSIRNSFLGSPRRHRKMVPTAEKMSLTPESSPELAKS- 594
121 LVEFVSQAOYPMHMAVYGNFQVHLHRLVINSFLTDSQGRGRGVNDLYRYKPLSSA 180
595 -----WFGNF--ISLDKEQIFLVLDK-----KPLSS-- 619
181 VVRNALAHVAKERELSWR--NSESFAMCRYGKREFKIGELRIQKOPYRLQIOLSAOR 238
620 -IKADIVAHFLSPSLSHSVLSQTSFRA-----EYKASGSPVFOKVRQVDISSE 671
239 S-----HTLEFQSLIEDLIMEKRRNDQIGRAAVLOELATHLHAPPEBED- 282
672 GPEPSRRDGGGGGIYSVTFLLISG---PSRRPKRVETIQAILSTHDQPSVQALADE 728
283 SNVART-----TPPGGRP-PAPSSSEEDG 305
729 KNGAQTRPAGAPPRSLQPPGPRDPPELSSSPRG 762

RESULT 13

US-10-803-277-2
Sequence 2, Application US/10803277

Patent No. 6919192
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Fridgde, Carl Johan
TITLE OF INVENTION: No. 6919192el Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0332-USA
CURRENT APPLICATION NUMBER: US/10/803,277
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: US/10/116,326
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,036
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 778
TYPE: PRT
ORGANISM: homo sapiens
US-10-803-277-2

Query Match 7.3%; Score 122; DB 2; Length 778;
Best Local Similarity 21.6%; Pred. No. 0.0017;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;

50 PPGPGGGLPDDGDDPPPO-----PPYDP----- 76
479 PSRCPGCGG---AGEOPPPSARSTPLPGPGSSSGTPLHSPHTPRASPTGTPTT 535
77 -----RLHEVCGSVFYRDECIYOKSFAPGSAALSTYTPENLTKCKPGD 120
536 PPSPGGCGVGAAMRSRLNSIRNSFLGSPRRHRKMVPTAEKMSLTPESSPELAKS- 594
121 LVEFVSQAOYPMHMAVYGNFQVHLHRLVINSFLTDSQGRGRGVNDLYRYKPLSSA 180
595 -----WFGNF--ISLDKEQIFLVLDK-----KPLSS-- 619

181 VVRNALAHVAKERELSWR--NSESFAMCRYGKREFKIGELRIQKOPYRLQIOLSAOR 238
620 -IKADIVAHFLSPSLSHSVLSQTSFRA-----EYKASGSPVFOKVRQVDISSE 671
239 S-----HTLEFQSLIEDLIMEKRRNDQIGRAAVLOELATHLHAPPEBED- 282
672 GPEPSRRDGGGGGIYSVTFLLISG---PSRRPKRVETIQAILSTHDQPSVQALADE 728
283 SNVART-----TPPGGRP-PAPSSSEEDG 305
729 KNGAQTRPAGAPPRSLQPPGPRDPPELSSSPRG 762

RESULT 14

US-08-801-742-4
Sequence 4, Application US/08801742

Patent No. 6359123
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: A NOVEL H-REV107-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,742
FILING DATE: Filed Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0200 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1709969
US-08-801-742-4

Query Match 7.0%; Score 116; DB 2; Length 160;
Best Local Similarity 31.9%; Pred. No. 0.00066;
Matches 38; Conservative 17; Mismatches 36; Indels 28; Gaps 6;

117 KPGDLVEFVSQAOYPMHMAVYGNFQVHL-----HRLVINSFLTDS----- 159
7 KPGDLIE-IRPMYSHMAIYGDGVITHLAPSEIPGAGAASJMSALTDAIYKKEILD 65
160 -QGRGRGVNDLY--RYKPLSSSAVVRNALAHVAKERELSWR--NSESFAMCRYG 211
66 VAGDKQVQVNNKHDETTPLPKTIQRAELVG---QEVLYRLTSNCEHFVIELRYG 121

```
QY 50 PPGPDGGLPDGDDGPPPO-----POPYD----- 76
D 463 PSRPRGGG---AGEQPPPSARSTPLPGPPGSRSSGGTPLHPLHTPRASPTGTGTT 519
QY 77 -----RLHEVECSVFRDECTIYOKSPAPGSAALSTYTPENTLNKCKPGD 120
D 520 PPPPGGCGVGAAMRSRLNSIRNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRS- 578
QY 121 LVEFVSAQYPMHVVYGNFQVHLHRLVINSFLTDASQGRGRVYNDLYRYKPLSSA 180
D 579 -----WFGNF--ISLDKEQIFVLKD-----KPLSS-- 603
QY 181 VERNALAHVGAKEBELSMR--NSESFAWCRYGKREKIGELRIGKOPYRLOQLSAQR 238
D 604 -IKADIVHAFSLPSLSHVSLSQTSFRA-----EYKASGSPSVFQKPVRFQVDISSSE 655
QY 239 S-----HTLEFOSLEDLIMEKRRNDQIGRAAVLQELATHLHPAPEEGD- 282
D 656 GPPSPRRDSSGGGGIYSVFTLLISG---PSRRFKRVVETIOQLSTHQPVSQALADE 712
QY 283 SNVART-----TPPGRP-PAPSSSEEDG 305
D 713 KNGAQTRPAGAPPRSLQPPCRPDELSSPRRG 746
RESULT 10
US-10-803-277-4
; Sequence 4, Application US/10803277
; Patent No. 6919192
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. 6919192el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/803,277
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/10/116,326
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 762
TYPE: PRT
ORGANISM: homo sapiens
US-10-803-277-4
Query Match 7.3%; Score 122; DB 2; Length 762;
Best Local Similarity 21.6%; Pred. No. 0.0016;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;
QY 50 PPGPDGGLPDGDDGPPPO-----POPYD----- 76
D 463 PSRPRGGG---AGEQPPPSARSTPLPGPPGSRSSGGTPLHPLHTPRASPTGTGTT 519
QY 77 -----RLHEVECSVFRDECTIYOKSPAPGSAALSTYTPENTLNKCKPGD 120
D 520 PPPPGGCGVGAAMRSRLNSIRNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRS- 578
QY 121 LVEFVSAQYPMHVVYGNFQVHLHRLVINSFLTDASQGRGRVYNDLYRYKPLSSA 180
D 579 -----WFGNF--ISLDKEQIFVLKD-----KPLSS-- 603
QY 181 VERNALAHVGAKEBELSMR--NSESFAWCRYGKREKIGELRIGKOPYRLOQLSAQR 238
D 604 -IKADIVHAFSLPSLSHVSLSQTSFRA-----EYKASGSPSVFQKPVRFQVDISSSE 655
QY 239 S-----HTLEFOSLEDLIMEKRRNDQIGRAAVLQELATHLHPAPEEGD- 282
D 656 GPPSPRRDSSGGGGIYSVFTLLISG---PSRRFKRVVETIOQLSTHQPVSQALADE 712
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QY 283 SNVART-----TPPGRP-PAPSSSEEDG 305
D 713 KNGAQTRPAGAPPRSLQPPCRPDELSSPRRG 746
RESULT 11
US-10-116-326-2
; Sequence 2, Application US/10116326
; Patent No. 6777545
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. 6777545el Human Kinases and Polynucleotides Encoding the S
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 778
TYPE: PRT
ORGANISM: homo sapiens
US-10-116-326-2
Query Match 7.3%; Score 122; DB 2; Length 778;
Best Local Similarity 21.6%; Pred. No. 0.0017;
Matches 72; Conservative 32; Mismatches 102; Indels 128; Gaps 14;
QY 50 PPGPDGGLPDGDDGPPPO-----POPYD----- 76
D 479 PSRPRGGG---AGEQPPPSARSTPLPGPPGSRSSGGTPLHPLHTPRASPTGTGTT 535
QY 77 -----RLHEVECSVFRDECTIYOKSPAPGSAALSTYTPENTLNKCKPGD 120
D 536 PPPPGGCGVGAAMRSRLNSIRNSFLGSPRHRKMQVPTAEEMSSLTPESSPELAKRS- 594
QY 121 LVEFVSAQYPMHVVYGNFQVHLHRLVINSFLTDASQGRGRVYNDLYRYKPLSSA 180
D 595 -----WFGNF--ISLDKEQIFVLKD-----KPLSS-- 619
QY 181 VERNALAHVGAKEBELSMR--NSESFAWCRYGKREKIGELRIGKOPYRLOQLSAQR 238
D 620 -IKADIVHAFSLPSLSHVSLSQTSFRA-----EYKASGSPSVFQKPVRFQVDISSSE 671
QY 239 S-----HTLEFOSLEDLIMEKRRNDQIGRAAVLQELATHLHPAPEEGD- 282
D 672 GPPSPRRDSSGGGGIYSVFTLLISG---PSRRFKRVVETIOQLSTHQPVSQALADE 728
QY 283 SNVART-----TPPGRP-PAPSSSEEDG 305
D 729 KNGAQTRPAGAPPRSLQPPCRPDELSSPRRG 762
RESULT 12
US-10-003-690-2
; Sequence 2, Application US/10003690
; Patent No. 6787345
; GENERAL INFORMATION:
; APPLICANT: Rony A.J. Curtis
; TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic Kinase
; FILE REFERENCE: NMI-206
; CURRENT APPLICATION NUMBER: US/10/003,690
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,893
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
```



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Db      67  -----GGSYPPPPSTGAAP-----PPGPAISLPEKAYT 98
QY      132 HW-----AAYVZGFQVHHLRLLEVINSLTDAQSGRGVNDLYRKKELSSAVRNAL 186
Db      99  FWTGRLAVLITONIPATVLLIGMLIOTLT-----KOEACVTDITOVNNOICATOPTG- 152
QY      187 AHVAKKEIELSWRNSESPAMCRVYGRKEFKIGELRIGK-----QPYRLQIQ 233
Db      153 --IGMAFWFAWLMATAYLWM--NYGYRGATGSS--IGTYMKFKVISEATGQPIGFMS 207
QY      234 IAGRSHTLEF-----QSLLEDLIM 252
Db      20  VVROLAHFVDAVICIGIFLPLMDSKRQTLADKIM 242

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RESULT 3

```

T00051
hypothetical protein KIAA0404 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00051
A:Shikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A.;
f:Submitted to the EMBL Data Library, October 1997
A:Description: Prediction of the coding sequences of unidentified human genes. VIII. The
A:Reference number: Z14080
A:Accession: T00051
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1956 <ISH>
A:Cross-references: UNIPROT:Q43154; UNIPARC:UP100000726E0; EMBL:AB007864; NID:d1175320;
A:Experimental source: brain, clone HG1236
C:Genetics:
A:Note: KIAA0404

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Query Match      6.1%; Score 102; DB 2; Length 1956;
Best Local Similarity 23.2%; Pred. No. 9.1; Indels 100; Gaps 14;
Matches 72; Conservative 24; Mismatches 114; Indels 100; Gaps 14;

QY      5  VEKLTILSYKEVPTADPTGVDGDDGPRIGVSYFSDNDEVDPPPPGPDGGGLPDGDD 64
Db      1312 LRELAPGSGHLPQAPISVYLFPGERSG-----PPSPVVG--PAGSL 1355
QY      65  GPPPPQPPYDPLRHEVCSVFYRDE-CIYOKSPAGSALSTYTPENLAKCKKPPDLVB 123
Db      1356 GSCSEKE--DEEEEGDGDITLDSDEFCLID--APG-LGIPRDEPVTQLHPPI-- 1407
QY      124 PVSQAQPRHMAVYVGFQVHHLRLLEVINSLTDAQSGRGVNDLYRKKELSSAVRN 183
Db      1408 -----VVRDQYFSRPIGSTDLK 1425
QY      184 NALAHVAKERELSWRNSESPAMCRVYGRKEFKIGELRIGKQF-YRLQIOLSAORSHTL 242
Db      1426 -APAHFPVSTRVLR--EVLVHMLYGGDF-----GPHRGHARTGSGPRSSPS 1474
QY      243 EFQSLLEDLIMEKKRNDQIGRA-AVLOELAT-----HLHPAREGSDNSVARTTPPGR 294
Db      1475 RCGSPRRPQNSWPTQCGSGRHHVLMELIOLSKVSPFHEVVPAPAPATG----- 1521
QY      295 PPAPSEED 304
Db      1522 PAAPSOELEB 1531

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RESULT 4

```

T00328
hypothetical protein KIAA0552 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00328
A:Shikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The completed

```

```

A:Reference number: Z14086; MUID:98290545; PMID:9628581
A:Accession: T00328
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-673 <NAG>
A:Cross-references: UNIPROT:Q60299; UNIPARC:UP10000139A8C; EMBL:AB011124; NID:g3043627
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0552

```

```

Query Match      6.1%; Score 101.5; DB 2; Length 673;
Best Local Similarity 22.6%; Pred. No. 2.4;
Matches 69; Conservative 35; Mismatches 106; Indels 95; Gaps 12;

```

```

QY      56  GGGLPDGGDPPPPPP--QYDPLRHEVCSVFYRDECIYOKSPAGSALSTYTP----- 110
Db      304 GGGLPFAACSPSPSALIOELERLMEKE-----DEVALARSLQSEALVAQVLEEROK 358
QY      111 -----NLNCKXKGDVVEFVSQAQPRHMAVYVGFQVHHLRLLEVINSLTDAQSGRR 163
Db      359 AMERELAEURQCS--GKLQAVARRAQ-----RAQGLQ 390
QY      164 GRVNDLYRKKELSSAVRNALAHVAKERELSWRNSESPAMCRVYGRKEF----- 215
Db      391 LQVLRHQDQKQLOSEA-----ALMRQREL-----EDKVAACQKQADLPRIETFK 439
QY      216 ---KIGELRIGKQPYR-----LQIOLSAQSHLEFQ-----SLEDLIM 252
Db      440 WEVCQKAGEISILKQOLKDSQADVQSKSEIVGRSLRQEGASLREKEQOLSLDSFS 499
QY      253 EKRRNDQIGR-----AAVLOELATHLPAREEG-----DSNVARTTPPPRPPAPSEED 304
Db      500 SKQASLEEGELPAKCLKPLATPVPAPFQDALTCESDEAKMRQAGVAAASLVSYD 559
QY      305 GEAVA 309
Db      560 GEAEA 564

```

RESULT 5

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T29266
hypothetical protein C01G8.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29266
R:Du, Z.; Gatlung, S.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid C01G8.
A:Reference number: Z20597
A:Accession: T29266
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-419 <DUZ>
A:Cross-references: UNIPROT:P91019; UNIPARC:UP1000017B712; EMBL:U80439; PIDN:AA837646.
A:Experimental source: strain Bristol N2; clone C01G8
C:Genetics:
A:Gene: C01G8.8
A:Map position: 1
A:Introns: 222/1; 285/3

```

```

Query Match      5.9%; Score 98; DB 2; Length 419;
Best Local Similarity 19.9%; Pred. No. 2.5;
Matches 67; Conservative 35; Mismatches 116; Indels 118; Gaps 12;

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```

QY      14  KEVPTADPTGVDG--PRIGVSYFSDNDE-----VEPPPPGPDGGGLPDGDDG 65
Db      147 KEGPNGNPATPSSSQPIPSASSIAESLDDKSGTYPAPQPPQ-----QH 195
QY      66  PPPPPQ-----PYDPLRHEVCSVFYRDECIYOKSPAGSALSTYTP-----NLNCK 115
Db      196 PPPPQQIMSPFPQAP-----SQATPSSSAASVAAPPTPKVSGVLSK 242
QY      116 CKPGD-----LVEFVSQAQPRHMAVYVGFQVHHLRLLEVI 151

```

